

STIC-Biotech/ChemLib

86502

Fr m: Davis, Minh-Tam
Sent: Tuesday, November 19, 2002 9:55 AM
To: STIC-Biotech/ChemLib
Subject: Search request for 09/878454

Please search in commercial database and in issued patent files:
SEQ ID NO:2, wherein positions 116-128 of SEQ ID NO:2 are mutated.

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

priority date

60, 210, 939

CREU 6/2000
of Fig 2

1. need xxx at 116 - 128
2. one x at 127

Point of Contact
Susan Hanley
Technical Info. Specialist
CM1 6B05 Tel: 305-4053

TYPE OF SEARCH:

Searcher: _____
Phone: _____
Location: _____
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NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
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Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CC CYTOPLASMIC DOMAIN.
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK.
 CC -1- TISSUE SPECIFICITY: UBQUITOUS.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC -----
 DR EMBL; U83236; AAB39758.1; -
 DR EMBL; U85611; AAB53387.1; -
 DR EMBL; U82226; AAC51106.1; -
 DR EMBL; AB021866; BAA36281.1; -
 DR EMBL; BC000846; AAH00846.1; -
 DR PDB; 1DGV; 08-DEC-99.
 DR Genew; HGNC:16920; CIB1.
 DR MIM; 602293; -
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 2.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat; 3D-structure.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF_HAND 2 (POTENTIAL).
 FT CONFLICT 44 44 T -> S (IN REF. 3 AND 5).
 SQ SEQUENCE 191 AA; 21717 MW; 9AA6EA7897881E55 CRC64;
 Query Match 100.0%; Score 962; DB 1; Length 191;
 Best Local Similarity 100.0%; Pred. No. 4.3e-70;
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSGRSLSKELLAAYQDLFLTKQELLAAHRRFCELLPQEQRTVESSLRAQVPFEQILS 60
 DB 1 MGSGRSLSKELLAAYQDLFLTKQELLAAHRRFCELLPQEQRTVESSLRAQVPFEQILS 60
 QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLVSFSDTPATPDIKSHYAFRIEDFDD 120
 DB 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLVSFSDTPATPDIKSHYAFRIEDFDD 120
 QY 121 GTLNREDLSRLVNCLTGEGEDTRLSASEMKOLIDNILESDIDRDGTINLSEFOHVISRS 180
 DB 121 GTLNREDLSRLVNCLTGEGEDTRLSASEMKOLIDNILESDIDRDGTINLSEFOHVISRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191
 RESULT 2
 KIP1_MOUSE STANDARD; PRT; 191 AA.
 AC Q9Z0F4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
 DE interacting protein) (kinase interacting protein) (KIP) (CIB).
 GN CIB1 OR PRKDCIP OR KIP OR CIB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;

RX MEDLINE=99069785; PubMed=9852683;
 RA Seki N., Hayashi A., Abe M., Araki R., Fujimori A., Fukumura R.,
 RA Hattori A., Kozuma S., Ohhira M., Hori T., Saito T.;
 RT "Chromosomal assignment of the gene for human DNA-PKcs interacting
 RT protein (KIP) on chromosome 15q25.3-q26.1 by somatic hybrid analysis
 RT and fluorescence in situ hybridization.";
 RL J. Hum. Genet. 43:275-277(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Fetal kidney;
 RX MEDLINE=99160477; PubMed=10051332;
 RA Saito T., Seki N., Hattori A., Hayashi A., Abe M., Araki R.,
 RA Fujimori A., Fukumura R., Kozuma S., Matsuda Y.;
 RT "Structure, expression profile, and chromosomal location of a mouse
 RT gene homologous to human DNA-PKcs interacting protein (KIP) gene.";
 RL Mamm. Genome 10:315-317(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Naik M.U., Naik U.P.;
 RT "Cloning and tissue distribution of murine calcium and integrin
 RT binding protein, CIB.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
 CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
 CC SIMILARITY).
 CC -1- TISSUE SPECIFICITY: UBQUITOUS.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC -----
 DR EMBL; AB006463; BAA74429.1; -
 DR EMBL; AB017361; BAA36165.1; -
 DR EMBL; AF173010; AAG38960.1; -
 DR EMBL; AK010345; BAB26868.1; -
 DR HSSP; Q99828; 1DGV.
 DR MGD; MGI:1344418; CIB1.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 2.
 DR ProDom; PD000012; EF-hand; 1.

DR SMART: SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF_HAND 2 (POTENTIAL).
 SQ SEQUENCE 191 AA; 21763 MW; C85B603A19F9D9AC CRC64;

Query Match 94.5%; Score 909; DB 1; Length 191;
 Best Local Similarity 94.2%; Pred. No. 7.2e-66;
 Matches 180; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 MGGSGSRLSKELLAEXODLFLTKQEILLAHRRFCCELLPOEORTVESSLRAQVFEQILS 60
 DB 1 MGGSGSRLSKELLAEXODLFLTKQEILLAHRRFCCELLPPEORTVESSLHTRVSFEQILS 60
 OY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLISVSDTATPDIKSHYAFRIEDFDD 120
 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLISVSDTATPDIKSHYAFRIEDFDD 120
 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKQILDNIIESDIDRDGTINLSEFQHVISRS 180
 DB 121 GTLDREDLSRLVNCITGEGEDTRLASASEMKQILDNIIESDIDRDGTINLSEFQHVISRS 180
 OY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 3
 KIP1_RAT
 ID KIP1_RAT STANDARD; PRT; 191 AA.
 AC 09R010;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
 interacting protein) (Kinase interacting protein) (KIP) (CIB).
 GN CIB1 OR PRKDCIP OR KIP OR CIB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99452760; Pubmed-10523297;
 Kauselmann G., Weiler M., Wulff P., Jessberger S., Konietzko U.,
 Scafidi J., Staubli U., Bereliter-Hahn J., Streibhardt K., Kuhl D.;
 "The polo-like protein kinases Fnk and Snk associate with a Ca(2+)-and
 integrin-binding protein and are regulated dynamically with synaptic
 plasticity.";
 EMBO J. 18:5528-5539(1999).

CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
 IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
 SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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DR EMBL; AF136585; AAF08368.1; -
 DR HSSP; Q99828; 1DGV.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 2.
 DR ProDom; PD000012; EF-hand; 1.

DR SMART: SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF_HAND 2 (POTENTIAL).
 SQ SEQUENCE 191 AA; 21800 MW; 3B0B0228879FCC7 CRC64;

Query Match 94.4%; Score 908; DB 1; Length 191;
 Best Local Similarity 94.2%; Pred. No. 8.7e-66;
 Matches 180; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 MGGSGSRLSKELLAEXODLFLTKQEILLAHRRFCCELLPOEORTVESSLRAQVFEQILS 60
 DB 1 MGGSGSRLSKELLAEXODLFLTKQEILLAHRRFCCELLPPEHRTVESSLHTRVSFEQILS 60
 OY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLISVSDTATPDIKSHYAFRIEDFDD 120
 DB 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLISVSDTATPDIKSHYAFRIEDFDD 120
 OY 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKQILDNIIESDIDRDGTINLSEFQHVISRS 180
 DB 121 GTLDREDLSRLVNCITGEGEDTRLASASEMKQILDNIIESDIDRDGTINLSEFQHVISRS 180
 OY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 4
 KIP2_MOUSE
 ID KIP2_MOUSE STANDARD; PRT; 187 AA.
 AC 09Z309;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kinase interacting protein 2 (KIP 2).
 GN KIP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain, and Testis;
 RX MEDLINE-99132027; Pubmed-9931475;
 Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Hori T.,
 Salto T.;
 "Structure, expression profile and chromosomal location of an isolog
 of DNA-PKcs interacting protein (KIP) gene.";
 Blochim. Biophys. Acta 1444:143-147(1999).

CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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DR EMBL; AB016080; BAA36545.1; -
 DR HSSP; Q99828; 1DGV.
 DR MGD; MGI:1929293; Kip2.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 3.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 157 168 EF_HAND 2 (POTENTIAL).
 SQ SEQUENCE 187 AA; 21703 MW; D21D21DCBDB6F5C CRC64;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 21, 2002, 17:57:51 ; Search time 31 Seconds
(without alignments)
1269.516 Million cell updates/sec

Title: US-09-878-454A-2
Perfect score: 962
Sequence: 1 MGSGSRLSKELLAEXQDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413	42.9	311	5	Q93640 caenorhabd1
2	369	38.4	185	11	Q9D9N5 mus musculu
3	346	36.0	187	4	Q96Q77 homo sapien
4	343.5	35.7	206	5	Q9W2Q5 drosophila
5	277	28.8	54	6	Q9GLJ2 sus scrofa
6	227.5	23.6	180	5	Q9GP83 dictyostell
7	206	21.4	175	5	Q9U0X7 leishmania
8	194	20.2	175	10	Q9LS47 arabidopsi
9	193	20.1	175	10	Q93VF2 eucalyptus
10	184.5	19.2	169	5	Q9NEN1 schistosoma
11	183.5	19.1	244	5	Q20804 caenorhabd1
12	182.5	19.0	189	5	Q9VNF9 drosophila
13	180.5	18.8	170	5	Q9NKM7 patinopecte
14	180.5	18.8	170	5	Q95P81 bombyx mori
15	177.5	18.5	115	11	Q99LQ9 mus musculu
16	176.5	18.3	187	5	Q9VWX8 drosophila

17	174	18.1	200	5	Q8SRF8 encephalit
18	171.5	17.8	175	3	Q9HDE1 cryptococcu
19	171.5	17.8	177	3	Q9HDD3 cryptococcu
20	171	17.8	274	10	Q9AWW4 oryza sativ
21	170.5	17.7	195	5	Q23643 caenorhabd1
22	170.5	17.7	213	5	Q16343 caenorhabd1
23	170.5	17.7	213	5	Q16343 caenorhabd1
24	170	17.7	170	4	Q8WYJ4 homo sapien
25	170	17.7	173	4	Q96L23 homo sapien
26	170	17.7	190	5	Q9NAY9 naegleria f
27	165.5	17.2	161	10	Q9AY39 oryza sativ
28	164.5	17.1	226	10	Q81446 arabidopsi
29	159	16.5	190	3	Q96X50 magnaporthe
30	159	16.5	190	3	Q8TGC0 magnaporthe
31	154	16.0	196	5	Q9N2Y1 caenorhabd1
32	154	16.0	225	10	Q8W5C8 oryza sativ
33	152.5	15.9	226	10	Q81447 arabidopsi
34	151.5	15.7	213	10	Q81445 arabidopsi
35	151	15.7	246	10	Q82641 arabidopsi
36	148	15.4	192	10	Q81328 arabidopsi
37	148	15.4	222	10	Q81223 arabidopsi
38	146	15.2	191	4	Q9UM19 homo sapien
39	141.5	14.7	153	5	Q9U5J0 trichomonas
40	141.5	14.7	160	5	Q9U5I9 trichomonas
41	141	14.7	220	4	Q9NS60 homo sapien
42	141	14.7	220	4	Q9HD11 homo sapien
43	141	14.7	220	11	Q9JM60 rattus norv
44	141	14.7	225	4	Q96K86 homo sapien
45	141	14.7	252	4	Q9NZ11 homo sapien

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT;	311 AA.
ID Q93640			
AC Q93640:			
DT 01-FEB-1997 (TREMBlrel. 02, Created)			
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)			
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
DE F30A10.1 protein.			
GN F30A10.1.			
OS Caenorhabditis elegans.			
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdittida; Rhabdittidae;			
OC Rhabdittidae; Peloderinae; Caenorhabditis.			
OX NCBI_Taxid=6239;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Barlow K.;			
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.			
RN [2]			
RP SEQUENCE FROM N.A.			
RX MEDLINE-99069613; PubMed-9851916;			
RA none;			
RT "Genome sequence of the nematode C. elegans: A platform for			
RT investigating biology."			
RL Science 282:2012-2018(1998).			
DR EMBL; Z81072; CAB03019.1; .			
DR HSSP; Q99828; IDGV.			
DR InterPro; IPR002048; EF-hand.			
DR Pfam; PF00036; efhand; 3.			
DR PRODOM; PD000012; EF-hand; 1.			
DR SMART; SM00054; Efh; 2.			
SO SEQUENCE 311 AA; 35960 MW; 97AF0AF56A6F526F CRC64;			
QY 1 MGSGSRLS-----KELLAEXQDLTFLTKQEILLAHRRFCCELLPOQRTVESS 48			
DB 111 MGNNASSLSELNLFSGKGVFTREQLDEYQDCFFTRKDIIRLYKRFYALNPHK---VPTN 167			
Query Match	42.9%;	Score 413;	DB 5; Length 311;
Best Local Similarity	42.5%;	Pred. No. 1.6e-28;	
Matches	88;	Conservative	41; Mismatches 52; Indels 26; Gaps 5;


```
QY      49 LNAQVP-----FEQIILSPELKANPFKERICRVSTSPAKDLSFEDFLDLLSVSDTA 102
        :: |         :::: :||| ||| ||| ||| : :|||:|||: |||: |
Db     168 MQGNRPATITLTTFEEVEKMPELKENPFKRRICEVS-EDGRGNLSFDDFLDMFSVSEMA 226
        :: |         :::: :||| ||| ||| ||| : :|||:|||: |||: |
QY     103 TPDIKSHYAIFDEDDDDGTINREDLSRLVNCLTGEGEDTRLASASEMKOLIDNILESDI 162
        :: |         :::: :||| ||| ||| ||| : :|||:|||: |||: |
Db     227 PLQLTKKYAFRIYDYDGDELGHDDLCKMIRSLTRD----ELSDVEVEFIETRIIEADL 282
        :: |         :::: :||| ||| ||| ||| : :|||:|||: |||: |
QY     163 DRDGTINLSEFQHVISRSPDFASSFKI 189
        | | :|| :||:||||||| : |
Db     283 DGDSSINFAEFEHVVSRSPPDFIRTFHI 309
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RESULT 2
Q9D9N5 PRELIMINARY; PRT; 185 AA.
ID Q9D9N5 AC Q9D9N5 DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
GN 1700041E2ORLK protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090; [1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=TESTIS;
RC MEDLINE=21085660; PubMed=11217851;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakai D., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Oikido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Humé D.A., Kamaya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001);
DR EMBL; AK006670; BAB24697.1; -
DR HSSP; Q99828; IDGV.
DR MGD; MG1:1920509; 1700041E2ORLK.
DR InterPro; IPRO02048; EF-hand.
DR InterPro; IPRO01125; Recoverin.
DR Pfam; PF00036; ehand; 2.
DR PRINTS; PR00450; RECOVERIN.
DR PRODOM; PD000012; EF-hand; 1.
DR SMART; SM00054; EfH; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
SQ SEQUENCE 185 AA; 21637 MW; 70C6B3EBF73844CB CRC64;

Query Match          38.4%; Score 369; DB 11; Length 185;
Best Local Similarity 44.2%; Pred. No. 6.le-25;
Matches      80; Conservative   37; Mismatches    50; Indels     14; Gaps

QY       11 ELAAEQDLFLTKQEILAHRRFCCELLPOEQRTVESSLRAGVPFEQIILSPELKANPEK 70
           | ||||| :||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db        12 EDLEEQALFTLTRNEITCIHDFTFLKLCPGSKHYKEATL----TMDQVSSLPALRVNPFR 67
           ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY       71 ERICRVSTSPAKDSLSEDFLDLLSVFSDDTPDPDIKSHYAIFEDFDGGTLNRREDLSR 130
           ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
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Dd    68 DRICRVFSHD---NVSESFEDVLGMASVFSEQACPSLKIEYAFRIYDFNENGFIIDEEDLEE   124
QY    131 LVNCLTGEGEDTRLBASE--MKQLIDNILEESDIDRDGTINLSEFOHVISRSPDEASSFK   188
      :| | : :| ||| | | : :||| | : :|||| :||
Db    125 IYERLL-KSDD----ASEDLMDVMHHVLSSEDLDNDMSLSFSFEHAMAKSPDENNSFR   179
QY    189 I 189
      |
Db    180 I 180
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RESULT 3
096Q77
ID Q96Q77 PRELIMINARY; PRT; 187 AA.
AC Q96Q77;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE KIP3.
GN KIP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hayashi A., Okaze H., Kozuma S., Saito T.;
RT "KIP3."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB050868; BAB71789.1; .
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; efhand; 3.
DR ProDom: PD000012; EF-hand; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_2.
SQ SEQUENCE 187 AA; 21801 MW; FB32CCB46DF5ADCF CRC64;

Query Match 36.0%; Score 346; DB 4; Length 187;
Best Local Similarity 39.9%; Pred. No. 6.7e-23;
Matches 77; Conservative 42; Mismatches 62; Indels 12; Gaps 4;

QY 1 MGGSGSRLSKELLA EYQDLTFLLTKQ EILLAHRRFC ELLPQ---EQTVESSLRAQVPFE 56
Db 1 MG NKQTVTFTH EQL EAYQDC TFFTRKEIMRLFYRYQDLAPQLVPLDYTTCPD--VKVPYE 57
QY 57 QILSLPELKANPFKERICRVFSTSPAKDSLSEDFDLDSVFSDTATPDIKSHYAFRIFD 116
Db 58 LIGSMPELKDNPFRQRIAYVS-EDGDGHMTLDNFLDMFSVMSENAPRDLKAYYAFKIYD 116
QY 117 FDDGTLNREDLSRLVNCITGEGEDTRLASASEMKQLIDNILEESDIDRDGTINLSEFOHV 176
Db 117 FNNDYICAMDLEQTVTKLTRGG---LSAEVSLVCEKVI DEADGDHDGRLSLDFQNM 172
QY 177 ISRSPDFASSFKI 189
Db 173 ILRAPDFLSTFHI 185

RESULT 4
09W205 PRELIMINARY; PRT; 206 AA.
AC Q9W205;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CG9236 protein.
GN CG9236.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.

```

RC STRAIN-BERKELEY;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaziel R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helit G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fostler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sidenkiamos I., Simpson M., Skupski M.P., Smith T.,
RA Splier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003452; AAF46635.1; .
DR HSSP; Q99828; IDGV.
DR FlyBase; FBgn0034558; CG9236.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 3.
DR ProDom; PD000012; EF-hand; 1.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; 2.
KW Calcium-binding.
SQ SEQUENCE 206 AA; 23591 MW; B3105F7F70F475A9 CRC64;

Query Match 35.7%; Score 343.5; DB 5; Length 206;
Best Local Similarity 44.3%; Pred. No. 1.3e-22;
Matches 78; Conservative 30; Mismatches 51; Indels 17; Gaps 5;

QY 17 QDITFLTKQEIILAHRRFCCLLPQ--EORTVESSLRAQVPEQILSLPELKANPFKERT 73
Db 43 KDCFFFTKREILRVHKRFRELRLPRLPRQMTGQASSVKVPCIEKPELR----- 94

QY 74 CRVSTSPAKDLSLSEDFLDLVSFSDTATPDIKSHYAFRIFFDDGDTLNREDLSRLVN 133
Db 95 -EAFSRD-GQGNLSFEDFLDALSVFSEQAPRDIKVFYAFKIYDFDQDGFIGHAD---LMS 149

QY 134 CLTGGEGDTRLASASEMKQLIDNILESDIDRDGTINTLSEFOHVISRSPDFASSFKI 189
Db 150 CLTTWTKN-ELSPHEHQIADKVEAEADVGDGKLSILEFEHYILRAPDLSTFHI 204

RESULT 5
Q9GLJ2 PRELIMINARY; PRT; 54 AA.
AC Q9GLJ2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE DNA-PK interaction-like protein (Fragment).
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith T.P.L., Fahrenkrug S.C., Rohrer G.A., Simmen F.A.,
RA Rexroad C.E. III, Keele J.W.;
RT "Mapping of Expressed Sequence Tags from a porcine early embryonic
RT cDNA library."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267715; AAG25931.1; .
DR HSSP; Q99828; IDGV.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 1.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 54
SQ SEQUENCE 54 AA; 6107 MW; 1A8057DE68A57A4A CRC64;

Query Match 28.8%; Score 277; DB 6; Length 54;
Best Local Similarity 98.1%; Pred. No. 1.7e-17;
Matches 53; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 102 ATPDIKSHYAFRIFFDDGDTLNREDLSRLVNCITGEGEDTRLASASEMKQLIDN 155
Db 1 ATPDIKSHYAFRIFFDDGDTLNREDLSQLVNCITGEGEDTRLASASEMKQLIDN 54

RESULT 6
Q9GP83 PRELIMINARY; PRT; 180 AA.
AC Q9GP83;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Calcineurin B.
GN CNBA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX-2;
RA Alichem A.;
RL Thesis (2000), Department of Fachbereich Biologie,
RL Universitaet Konstanz, Konstanz, Germany.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX-2;
RA Alichem A.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ301668; CAC20026.2; .
DR HSSP; P06705; LAUI.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
SQ SEQUENCE 180 AA; 20739 MW; E2E947E8D280D0B6 CRC64;

Query Match 23.6%; Score 227.5; DB 5; Length 180;
Best Local Similarity 29.8%; Pred. No. 1.8e-12;
Matches 53; Conservative 44; Mismatches 66; Indels 15; Gaps 4;

QY 1 MGGSGRLSKELLAAYODLFTLTKQEIILAHRRFCCLLPQEQRTVESSLRAQVPEQILS 60
Db 1 MGGSGRLSKELLAAYODLFTLTKQEIILAHRRFCCLLPQEQRTVESSLRAQVPEQILS 60

```
Db 1 MGNQHSLNKEOLEQMKDNSSFSSEAEKLYRRFQMLDKDGSGLT-----DEFLS 52
QY 61 LPELKANPFEKRICRVSTSPAKDS-LSFEDFLDLVSFSDTATPDIKSHYAFRIEDFD 119
Db 53 IPDLALNPLEERVIQIFDQ--KNEIEFSEFVGTLATLSHKGTKEKFLFQIYDIDC 110
QY 120 DGTLNREDLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 177
Db 111 DGFISNGELEFQVKMVG---TNLNDVQLQOIVDKTIIIEGDKDKGISDEFIHMI 164

RESULT 7
Q9UOX7 PRELIMINARY; PRT; 175 AA.
AC Q9UOX7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Calcineurin subunit.
GN L7171.06.
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_Taxid=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RX Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M., Smith D.F.;
RA "A physical map of the Leishmania major Friedlin genome.";
RT Genome Res. 8:135-145(1998).
RL EMBL; AL13435; CAB62809.1; -
DR HSSP; P06705; LAUI.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
SQ SEQUENCE 175 AA; 19660 MW; 9448F127F4DFA0EB CRC64;

Query Match 21.4%; Score 206; DB 5; Length 175;
Best Local Similarity 25.8%; Pred. No. 1.4e-10;
Matches 47; Conservative 44; Mismatches 77; Indels 14; Gaps 4;

QY 8 LSKELLAEXODLFLTKOELLAHRRFCELLPOEQRTESSLAQVPEQILSPELKAN 67
Db 6 LTAELONIRESTALTDAQVQRLYKFSKL-----NKDKSGKITRAEFNSIPALASN 57
QY 68 PFEKRICRVSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIEDFDGTLNRED 127
Db 58 PLVDRLVLAAMDTD-GDSTVDEGDFVRALAVLSSATSKEKDLRFTFKMYDVGDRISNKD 116
QY 128 LSRVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVSRSPDFASSF 187
Db 117 LFGMLSIMVG---VNLQOMQLQOIVDKTIEADVDRDGYTFEEFQ-ALAVNSDFGRL 171
QY 188 KI 189
Db 172 NL 173

RESULT 8
Q9LS47 PRELIMINARY; PRT; 175 AA.
ID Q9LS47
AC Q9LS47;
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DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Calcineurin b subunit (Protein phosphatase 2b regulatory subunit)-like
DE protein (Hypothetical 20.0 kDa protein).
GN AT3G18430.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Natusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene At3g18430 (GI:15229640).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Natusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA EMBL; AB026658; BAB01109.1; -
DR EMBL; AY063789; AAL36096.1; -
DR EMBL; AY091287; AAM14226.1; -
DR HSSP; P06705; LAUI.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 2.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 175 AA; 20032 MW; B26D6F2ADA26AFED CRC64;

Query Match 20.2%; Score 194; DB 10; Length 175;
Best Local Similarity 27.2%; Pred. No. 1.6e-09;
Matches 50; Conservative 45; Mismatches 65; Indels 24; Gaps 5;

QY 1 MGSGRSLSKELLAEXQ---DLFLTKOELLAHRRFCELLPOEQRTESSLAQVPE 56
Db 1 MGNITSSMLTYDIEEVQSHCHDL--FEQOEILSLYQRFQCL-----DRNAKFISAD 50
QY 57 QILSLPELKANPFEKRICRVSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIED 116
Db 51 EFLSVPEFAMNPLSQRLKLV-----DGLNFKDFAVFLSAFSAKASLRQKVLIFKVVYD 104
QY 117 FDDGTLNREDLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 176
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[illegible]

RESULT 9

ID	Q93VF2	PRELIMINARY;	PRT;	175 AA.
AC	Q93VF2;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, last annotation update)			
DE	Calcineurin-like protein.			
GN	ECB1 OR ECB1.			
OS	Eucalyptus camaldulensis (Murray red gum), and Eucalyptus grandis.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Oxosids II; Myrtales; Myrtaceae; Eucalyptus.			
OX	NCBI_TaxID=34316, 71139;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=E.camaldulensis, and E.grandis; TISSUE=FLOWER;			
RA	Falibairn D.J., Gomez-Gallego S., Sawbridge T., Teasdale R.D.;			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF197334; AAL25650.1; -			
DR	EMBL; AF197330; AAL25647.1; -			
DR	InterPro: IPR002048; EF-hand.			
DR	Pfam: PF00036; EF-hand; 2.			
DR	ProDom: PD000012; EF-hand; 1.			
DR	PROSITE: PS00018; EF-HAND; UNKNOWN_1.			
SO	SEQUENCE 175 AA; 1997 MW; C4E773EE42A3EEF16 CRC64;			

Query

Best Local Similarity 26.4%; Pred. NO. 2e-09;
Matches 48; Conservative 45; Mismatches 69; Indels 20; Gaps 4;

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QY 1 MCGSGSRLSKELLAEYQD--LTFLTQOEILLAHRRCELLPOEQRTVSSLRQVPFEQI 58
   | | : | : : | | : : : : : | : : : : :
Db 1 MGNASSMLTQYDIEEYQDHCNNLFSSQOEIVSLYERFCQL-----DRNAKGFISADEF 52

QY 59 LSPLELKANPFKERICRYESTSPAKDSLSEFEDFLDLLSVESDTPATPDIKSHYAFRIEFD 118
   | | : | : : : : | | : : : | | : : : | |
Db 53 LSYPEFAMNPLSQRLKMY-----DGLNFKEDFAFLSAFSAKASKQOKTELIFKYYDSD 106

QY 119 DDGTLNREDLSRLVNCLTGEGEDTRLASASEMKQLDNLILESDIDRDGTINLSEFQHAVIS 178
   : | : : : : : : : : : : : : : : : : : :
Db 107 CNGKVSFNDILEVLRDLISG---PFMSDEQREQVLVQVLKEAGYTRRESYLLDDFVKVFG 162

QY 179 RS 180
   |
Db 163 NS 164

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RESULT 1

ID	Q9NEN1	PRELIMINARY;	PRT;	169 AA.
MAC	Q9NEN1;			
DDT	01-OCT-2000	(TREMBLrel. 15, Created)		
DDT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)		
DDT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)		
DDE	Calcineurin B.			
DOS	Schistosoma mansoni (Blood fluke).			
OOC	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;			
OOC	Schistosomatoidae; Schistosomatidae; Schistosoma.			
DCX	NCBI_TaxID=6183;			
RN	[1]			
RRP	SEQUENCE FROM N.A.			
RRP	MEDLINE=20520966; PubMed=11071287;			
RFX	Mecozzi B., Rossi A., Lazaretti P., Kady M., Kaiser S., Valle C.,			

RA Clotl D.; Klinkert M.Q.;
RT "Molecular cloning of Schistosoma mansoni calcineurin subunits and
RT immunolocalization to the excretory system."
RL Mol. Biochem. Parasitol. 110:333-343(2000).
DR EMBL; AJ276885; CAB93677.1; .
DR HSSP; P06705; LTCO.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 169 AA; 19137 MW; 878E01D08BC5DC1D CRC64;

Query Match

Best Local Similarity 30.18; Pred. No. 1.1e-08;
Matches 37; Conservative 32; Mismatches 49; Indels 5; Gaps 2

QY	56	EQLSPELKPANPFKERICRVSTSPAKDLSFEDEFLDLLSVESDTATPDIKSHYAFRIF	115
	:	: : : : : + :	: : : : :
Dd	40	KEFMSLEPQLQNPLVARVIEIFPD-GNGEVDFFEKFINMSGQSAGKEAKLKFAFKIY	98
QY	116	DFDDGTLNREDLSRLVNCLTGEGBDTRLASASEMKOLIDNILESDIDRDGTINLSEFH	175
		: : : : : :	: : : : :
Dd	99	DMKDGYISNGELFQVLKMMVG-----NNLKTQLQQIVDKTIMFPDKDEDGRISFEETCE	154
QY	176	VIS 178 .	
	:	:	
Dd	155	VVS 157	

RESULT 11

ID	Q20804	PRELIMINARY;	PRT;	244 AA.
AC	Q20804;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	F55C10.1 protein.			
GN	F55C10.1.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Peloderinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Dobson R.;			
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99069613; PubMed=9851916;			
RA	none;			
RT	"Genome sequence of the nematode C.elegans: A platform for			
RT	investigating biology.";			
RL	Science 282;2012-2018(1998).			
DR	EMBL; Z74036; CAA98489.2; .			
DR	HSSP; P06705; LAUI.			
DR	InterPro; IPR002048; EF-hand.			
DR	InterPro; IPR001125; Recoverin.			
DR	Pfam; PF00036; efhand; 4.			
DR	PRINTS; PR00450; RECOVERIN.			
DR	ProDom; PD000012; EF-hand; 2.			
DR	SMART; SM00054; EFh; 4.			
DR	PROSITE; PS00018; EF_HAND; UNKNOWN_4.			
QO	SEQUENCE 244 AA; 27901 MW; 6B99CB58CB77D08B CRC64;			

Query Match

Best Local Similarity 27.8%; Pred. NO. 2.le-08;
Matches 50; Conservative 38; Mismatches 69; Indels 23; Gaps 6;

QY 3 GSGSRLSKELLAEO--DITFLTKQEILLAHRRCEELLPGEORTVSSLRQVPFEQILS 60
|:::| |:::| :|| |||:| |:::|


```

Db      75  GADASLPMEGMSNFDAYELRLTT-----RRFKKL-----DVDGS--GSLSVEEFMS 118
Qy      61  LPELKANPERKICRVFSTSPAKDSIFEDELDSLVSFSDTATPDIKSHYAFRIEFDDED 120
         ||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     119  LPELQCNPLVQVRVIDFD-EDNGEYDFREFIQISQFSVKGDKNFKLKAFAFIYDMRD 177
         |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy     121  GTLNREDLSRLVNCLTGEGEDTRLASSEMKOLLIDNILEESDIDRDGTINLSEFQHVISRS 180
         |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     178  GFISNGELFQYLKMWG-----NNLKDSQLQIQIVDKTILFHDKRDGDGKISFOEFCDVHE 233
         |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 12
Q9VNF9
ID      Q9VNF9      PRELIMINARY;      PRT;      189 AA.
AC      Q9VNF9;
DT      01-MAY-2000 (TREMBlrel. 13, Created)
DT      01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT      01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE      CG2185 protein (LD19356p).
GN      CG2185.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BERKELEY;
RX      MEDLINE-20196006; PubMed-10731132;
RA      Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA      Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA      George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA      Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA      Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,
RA      Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA      Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA      Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA      Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,
RA      Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA      Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA      Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA      de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA      Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA      Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA      Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA      Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA      Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA      Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA      Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA      Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA      Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA      Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA      Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA      Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA      Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA      Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA      Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA      Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA      Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA      Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA      Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA      Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA      Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA      Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA      Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA      "The genome sequence of Drosophila melanogaster.";
RA      science 287:2185-2195(2000).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BERKELEY;
RA      Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA      Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA      Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

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[illegible]

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RESULT 13
O9NKM7
ID O9NKM7 PRELIMINARY; PRT; 170 AA.
AC O9NKM7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Calcineurin B.
OS Patinopecten yessoensis (Ezo giant scallop) (Yesso scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
OC Pectinoidea; Pectinidae; Mizunopecten.
OX NCBI_TaxID=6573;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Uryu M., Nakatomi A., Watanabe M., Hatsuse R., Yazawa M.;
RT "Molecular Cloning of cDNA Encoding Two Subunits of Calcineurin from
RT Scallop Testis: Demonstration of Stage-Specific Expression during
RT Maturation of the Testis.";
RL J. Biochem. 0:0-0(2000).
DR EMBL; AB041524; BAA94543.1; -.
DR HSSP; P06705; IAU.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 170 AA; 19238 MW; 9450322698470F44 CRC64;

Query Match 18.8%; Score 180.5; DB 5; Length 170;
Best Local Similarity 25.1%; Pred. No. 2.4e-08;
Matches 44; Conservative 42; Mismatches 70; Indels 19; Gaps 4;

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D_b 2 GNENSLPMELCSNFD-----PDEIKRLGKR-----RKILDNSGSLSYDEFMTLP 47

QY 63 ELKANPEKERICRVSTSPAKDLSFEDELDDLVSFSDTATPDIKSHYAFRIFEDFDDGT 122
 || : || : | : : : : : | : : : : | : |
Db 48 ELQQNPVQRVIDIEDTD-GNGEYDFKEFIEGVSOFSVKGGKLSKLRFAFKIYDMDKGY 106

QY 123 LNREDSLRYNCLTGEGEDTRLASSEMQLIDNILESDDIRDTINTLSEFGHVI 177
 :: :| :: : | : : : : : | : : | | | : | : | :
Db 107 ISNGELCYLKMAVG----NNLKDTQLQIYDKTIIHADADGDGKISFEFCAYV 157

RESULT 14

ID	Q95P81	PRELIMINARY;	PRT;	170 AA.
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DT	01-DEC-2001 (TREMBlrel. 19, (reated)
DT	01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT	01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE	Calcineurin B.
GN	CNB.
OS	Bombyx mori (Silk moth).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC	Bombycoidea; Bombycidae; Bombyx.
OX	NCBI_TaxID=7091;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SHUKO X RYUHAKU; TISSUE=PHEROMONE GLAND;
RA	Yoshiiga T., Matsumoto S.;
RT	"cDNA cloning of heterosubunits of calcineurin from pheromone gland of
RT	Bombyx mori.";
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AF2872251; AAK83039.1; -.
DR	InterPro: IPR002048; EF-hand.
DR	Pfam: PF00036; ehand; 4.
DR	ProDom: PD000012; EF-hand; 2.
DR	PROSITE: PS00018; EF_HAND; UNKNOWN 4.
SO	SEQUENCE 170 AA; 19357 MW; 5ECC15B820097130 CRC64;

Query Match	18.8%;	Score 180.5;	DB 5;	Length 170;
Best Local Similarity	24.7%;	Pred. No. 2.4e-08;		
Matches 44;	Conservative 44;	Mismatches 71;	Indels 19;	Gaps 4;

```

QY 3 GSGSRLSKELLAEYODTLFTLKQOEIILAHRRFCCELLPQOEQRTVESSLRAQVPFEQILSLP 62
    | : : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 2 GNENSIPMELCSNFD-----ADEIRRLGKR-----RKLDLDNSGALSIDEFMSLP 47

QY 63 ELKANPFKERICRVFSTSPAKDSLSEDFLDLLSVFSDTATPDIKSHYAFRIEFDDEDT 122
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 48 ELQONPLVQRYIDIFD-ADGNGEVDEKEFIQGVSQFSYKGDKLSKLRFARFYDMNDGCF 106

QY 123 LNREDLSRYNCLTGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFQHVISR 180
    : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 107 ISNGELFYVKMVG-----NNLKQDLOQIVDKTILFADKDEGDKISFEFCNVAGNT 160

```

RESULT 15

099109

ID	Q99LQ9	PRELIMINARY;	PRT;	115 AA.
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DT	01-JUN-2001 (TREMBLrel, 17, Created)
DT	01-JUN-2001 (TREMBLrel, 17, last sequence update)
DT	01-MAR-2002 (TREMBLrel, 20, last annotation update)
DE	Hypothetical 13.1 kDa protein.

GN PPP3R1.

Mus musculus (mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

Submitted (JAN-2001) to the EMBL/GenBank/MDBI databases

DR EMBL; BC002267; AAH02267.1; -.
DR HSSP; P06705; LAUI.
DR MGD; MGI:107172; Pp3r1.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 3.
DR PRINTS; PR00450; RECOVERIN.
DR PRODOM; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
DR Hypothetical protein.
KW SEQUENCE 115 AA; 13134 MW; B3E1734C07A65471 CRC64;
SQ

Query Match	18.58;	Score 177.5;	DB 11;	Length 115;
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Best Local Similarity 31.38; Pred. No. 2.7e-08;

Matches	36;	Conservative	30;	Mismatches	44;	Indels	5;	Gaps.	2;
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```
QY 59 LSPELKANPEKERICRVSTSPAKDSUSEDEFLDLSVSFSDTATPDIKSHYAFRIEDED 118
    :||||: || :|| :|:|:|:|:| || :| :||||:| |
Db 1 MSLPELQONPLVQRVIDIFEDF-GNGEYDFKEFIEGVSGFSVKGDKEQKLREAFRIYMD 59
```

QY 119 DGGTLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNILEESDIDRDGTINSEF 173
||:::||::|:::||||::|||::||
Db 60 KDGYSNGELPQLKMAVG---NNLKDTQLQIIVDKTIINADKKDDGRISFEFF 110

Search completed: November 21, 2002, 17:58:51
Job time : 33 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 21, 2002, 17:57:51 ; Search time 15 Seconds
(without alignments)
374.652 Million cell updates/sec

Title: US-09-878-454A-2

Perfect score: 962
Sequence: 1 MGGSGSRLSKELLAEXODLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	958	99.6	191	4	US-08-720-625-2 Sequence 2, Appl1
2	952	99.0	191	3	US-08-764-563-1 Sequence 1, Appl1
3	216.5	22.5	177	3	US-08-764-563-3 Sequence 3, Appl1
4	204.5	21.3	174	1	US-08-328-322-17 Sequence 17, Appl1
5	193.5	20.1	157	1	US-08-328-322-15 Sequence 15, Appl1
6	186.5	19.4	169	4	US-08-720-625-4 Sequence 4, Appl1
7	186.5	19.4	170	3	US-08-764-563-5 Sequence 5, Appl1
8	176	18.3	186	3	US-08-555-352-8 Sequence 8, Appl1
9	176	18.3	186	4	US-09-257-825B-8 Sequence 8, Appl1
10	176	18.3	186	4	US-09-257-825B-8 Sequence 8, Appl1
11	172.5	17.9	179	3	US-08-764-563-4 Sequence 4, Appl1
12	153.5	16.0	196	3	US-09-048-889-1 Sequence 1, Appl1
13	150	15.6	193	3	US-08-655-352-3 Sequence 3, Appl1
14	150	15.6	193	4	US-09-258-016-3 Sequence 3, Appl1
15	150	15.6	193	4	US-09-257-825B-3 Sequence 3, Appl1
16	146	15.2	220	4	US-09-399-913-26 Sequence 26, Appl1
17	146	15.2	220	4	US-09-298-731-26 Sequence 26, Appl1
18	142	14.8	191	3	US-08-655-352-7 Sequence 7, Appl1
19	142	14.8	191	4	US-09-258-016-7 Sequence 7, Appl1
20	142	14.8	191	4	US-09-257-825B-7 Sequence 7, Appl1
21	141	14.7	220	4	US-09-399-913-24 Sequence 24, Appl1
22	141	14.7	220	4	US-09-298-731-24 Sequence 24, Appl1
23	141	14.7	252	4	US-09-399-913-20 Sequence 20, Appl1
24	141	14.7	252	4	US-09-298-731-20 Sequence 20, Appl1
25	141	14.7	270	4	US-09-399-913-14 Sequence 14, Appl1
26	141	14.7	270	4	US-09-298-731-14 Sequence 14, Appl1
27	139	14.4	193	3	US-08-655-352-2 Sequence 2, Appl1

28	139	14.4	193	4	US-09-258-016-2	Sequence 2, Appl1
29	138	14.3	193	4	US-09-257-825B-2	Sequence 2, Appl1
30	138	14.3	216	4	US-09-399-913-6	Sequence 6, Appl1
31	138	14.3	216	4	US-09-298-731-6	Sequence 6, Appl1
32	138	14.3	227	4	US-09-399-913-8	Sequence 8, Appl1
33	138	14.3	227	4	US-09-399-913-10	Sequence 10, Appl1
34	138	14.3	227	4	US-09-298-731-8	Sequence 8, Appl1
35	138	14.3	227	4	US-09-298-731-10	Sequence 10, Appl1
36	138	14.3	245	4	US-09-399-913-4	Sequence 4, Appl1
37	138	14.3	245	4	US-09-298-731-4	Sequence 4, Appl1
38	138	14.3	270	4	US-09-399-913-18	Sequence 18, Appl1
39	138	14.3	270	4	US-09-298-731-18	Sequence 18, Appl1
40	137	14.2	216	4	US-09-399-913-2	Sequence 2, Appl1
41	137	14.2	216	4	US-09-298-731-2	Sequence 2, Appl1
42	136	14.1	225	4	US-09-399-913-30	Sequence 30, Appl1
43	136	14.1	225	4	US-09-298-731-30	Sequence 30, Appl1
44	136	14.1	252	4	US-09-399-913-22	Sequence 22, Appl1
45	136	14.1	252	4	US-09-399-913-28	Sequence 28, Appl1

ALIGNMENTS

RESULT 1
US-08-720-625-2
Sequence 2, Application US/08720625
Patent No. 6242587
GENERAL INFORMATION:
APPLICANT: Naik, Ulhas P.
APPLICANT: Parise, Leslie V.
TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: NO. 6242587th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,625
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-625-2

Query Match 99.6%; Score 958; DB 4; Length 191;
Best Local Similarity 99.5%; Pred. No. 1.6e-97;
Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAEXODLTFLTKOEILLAHRRFCCLLPQEQRTVESSLRAQVPEQILS 60
|||||
Db 1 MGGSGSRLSKELLAEXODLTFLTKOEILLAHRRFCCLLPQEQRSVSSLRAQVPEQILS 60
|||||
QY 61 LPELKNPFKERICRVSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRTFDDDD 120
|||||

Db 61 LPELKANPEKERICRVSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIEFDDE 120

OY 121 GTLNREDLSRLVNCITGEGEDTRLSASEMKQIDNILEESDIDRDGTINLSEFQHVISR 180

Db 121 GTLNREDLSRLVNCITGEGEDTRLSASEMKQIDNILEESDIDRDGTINLSEFQHVISR 180

OY 181 PDFASSFKIVL 191

Db 181 PDFASSFKIVL 191

RESULT 2

US-08-764-563-1

Sequence 1, Application US/08764563

Patent No. 6093565

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Goli, Surya K.

TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/764,563

FILING DATE: Herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0178 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 191 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: Consensus

CLONE: Consensus

US-08-764-563-1

Query Match 99.0%; Score 952; DB 3; Length 191;

Best Local Similarity 99.0%; Pred. No. 7.2e-97;

Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MGGSGSRLSKELLAEOYDLFTLKQETLLAHRFCCELLPOORTVESSLRAQVPFEQILS 60

Db 1 MGGSGSRLSKELLAEOYDLFTLKQETLLAHRFCCELLPOORTVESSLRAQVPFEQILS 60

OY 61 LPELKANPEKERICRVSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIEFDDE 120

Db 61 LPELKANPEKERICRVSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIEFDDE 120

OY 121 GTLNREDLSRLVNCITGEGEDTRLSASEMKQIDNILEESDIDRDGTINLSEFQHVISR 180

Db 121 GTLNREDLSRLVNCITGEGEDTRLSASEMKQIDNILEESDIDRDGTINLSEFQHVISR 180

OY 181 PDFASSFKIVL 191

Db 181 PDFASSFKIVL 191

RESULT 3

US-08-764-563-3

Sequence 3, Application US/08764563

Patent No. 6093565

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Goli, Surya K.

TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/764,563

FILING DATE: Herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0178 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 177 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 458230

US-08-764-563-3

Query Match 22.5%; Score 216.5; DB 3; Length 177;

Best Local Similarity 29.2%; Pred. No. 4.1e-16;

Matches 52; Conservative 40; Mismatches 73; Indels 13; Gaps 3;

OY 1 MGGSGSRLSKELLAEOYDLFTLKQETLLAHRFCCELLPOORTVESSLRAQVPFEQILS 60

Db 1 MGTNTSSLRPEEVEEMQKGTNETQETIKKLYKRFKKLDKDGNGTISK-----DEFLM 52

OY 61 LPELKANPEKERICRVSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIEFDDE 120

Db 53 IPELAVNPVLRKVISIFDEN-GDGSVNFKEFIALSVFNAQGDQKRLFAFKVYDIDGD 111

OY 121 GTLNREDLSRLVNCITGEGEDTRLSASEMKQIDNILEESDIDRDGTINLSEFQHVISR 178

Db 112 GYISNGELFTVLKMGV-----NNLSDVQLOQIVDKTILAEADGDGKISFEFAKTLS 165

RESULT 4

US-08-328-322-17

Sequence 17, Application US/08328322

Patent No. 5723436
GENERAL INFORMATION:
APPLICANT: Huang, Laiqiang
APPLICANT: Cyert, Martha S.
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,322
FILING DATE: 24-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: P38,615
REFERENCE/DOCKET NUMBER: 8600-0151.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-322-17

Query Match 21.3%; Score 204.5; DB 1; Length 174;
Best Local Similarity 27.1%; Pred. No. 8.2e-15;
Matches 48; Conservative 44; Mismatches 68; Indels 17; Gaps 4;

QY 1 MGGSGRLSKELLAAYQDLFTLTKQELLAHRRFCELLPQEQRTVESSLRAQVFEQILS 60
DB 1 MGAAPSKIYDGLLED---TNRDREIERLRKRFMKLDRDSSGSIDKN-----EFMS 48

QY 61 LPELKANPFKERICRVSTSPAKDSLFEFELDLISVSDTATPDIKSHYAFRIFEDDD 120
DB 49 IPGVSSNPLAGRIMEVFADNSGD-VDFQEFITGLSIFSGRSGKDEKLRFKITYDIDKD 107

QY 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILESDIDRDGTINLSEFQHV 177
DB 108 GFISNGELFYLKIMVG---SNLDEQLQIIVDRITVENSDSDGRLSFEFKNAT 160

RESULT 5
US-08-328-322-15
Sequence 15, Application US/08328322
Patent No. 5723436
GENERAL INFORMATION:
APPLICANT: Huang, Laiqiang
APPLICANT: Cyert, Martha S.
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,322
FILING DATE: 24-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: P38,615
REFERENCE/DOCKET NUMBER: 8600-0151.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-322-15

Query Match 20.1%; Score 193.5; DB 1; Length 157;
Best Local Similarity 27.3%; Pred. No. 1.1e-13;
Matches 42; Conservative 40; Mismatches 59; Indels 13; Gaps 3;

QY 24 KQELLAHRRFCELLPQEQRTVESSLRAQVFEQILSPELKANPFKERICRVSTSPAK 83
DB 3 RDEIERLRKRFMKLDRDSSGSIDKN-----EFMSIPGVSSNPLAGRIMEVFADNSG 54

QY 84 DLSFEDFLDLISVSDTATPDIKSHYAFRIFEDDDGTNLNREDLSRLVNCITGEGEDTR 143
DB 55 D-VDFQEFITGLSIFSGRSGKDEKLRFKITYDIDKDFISNGELFYLKIMVG-----SN 109

QY 144 LSASEMKQLIDNILESDIDRDGTINLSEFQHV 177
DB 110 LDDEQLQIIVDRITVENSDSDGRLSFEFKNAT 143

RESULT 6
US-08-720-625-4
Sequence 4, Application US/08720625
Patent No. 6242587
GENERAL INFORMATION:
APPLICANT: Naik, Uthas P.
APPLICANT: Parise, Leslie V.
TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6242587th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,625
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 4:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acid
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-720-625-4

```

Query Match	19.48;	Score 186.5;	DB 4;	Length 169;
Best Local Similarity	31.18;	Pred. No. 7.5e-13;		
Matches 38;	Conservative 32;	Mismatches 47;	Indels 5;	Gaps 2;

Dy 56 EQILSPELKPANPFKERICRVESISPAKDSLSFEDELLDLSVESDTATPDIKSHYAFRIE 115
| : ||||| : | : | : ||||| : | : |||||
Db 40 EEFMSLELOQNPVQRVIDIFEDF-GNGEVDFKEFIIEGVSSFSVKGDKEOKLRFAFRIT 98

QY 116 DEDDDGTLNREDLSRLVNCLTGEGEDTRLASASEMKOLIDNLTIEESDIDRDGTINLSEQH 175
 | | | | : : : : | : : : : | | | : |
 Db 99 DMDKDGYSNGELFQVLKMYG----NNLKDTQLQIVDKITLINADKGDGRISFEFECA 154

QY	176	VI	177
		↓	
Db	155	VV	156

RESULT 7
US-08-764-563-5

```

: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Goll, Surya K.
: TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304

```

```

: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: Fastseq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/764,563
: FILING DATE: Herewith
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
:

```

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36, 749
REFERENCE/DOCKET NUMBER: PF-0178 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 170 amino acids

TYPE: amino acid

STIKANDELNESS: 31

LOGPOLY: linear

LIBRARY. GenBank

CLONE: 461682

US-08-764-563-5

Query Match

19.48; Score 186.5; DB 3; Length 170;

Best Local Similarity 31.1%; Pred. No. 7.6e-13;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;

```
QY      56 EQILSLPELKANPFKERICRVSTSPADSUSFEFDLLSVFSDTATPDIKSHYAFRIF 115
        | : :| | | | : : : : | : : : : : : : : : : : : : : : : : : :
Db      41 EEFMSLPQLQNPLVQRVIDIFTD-GNEEVDKFKEFIGVSQSFSYKGDKEOKLRFAFRIV 99
```

QY 116 DFDDDGTLNRDLSRLVNCLTGEGEDTRLSASEMKOLIDNILEESIDIRDTINLSEFQH 175
| | | : : : : | : : : : : : : : : :
Db 100 DMDKGYISNGELFQVLKMVG---NNLKDTQLQQIVDKTIINDKKGDGGRISFEFFCA 155

QY	176	VI	177
		↓:	
Db	156	VV	157

RESULT 8
US-08-655-352-8
; Sequence 8, Application US/08655352
; Patent No. 6077991

GENERAL INFORMATION:
APPLICANT: Bachettira W. Pooviah, Zhihua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
NUMBER OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESS: Klargust Sparkman Cam
ADDRESSEE: Winston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204

```

:      COMPUTER READABLE FORM:
:      MEDIUM TYPE: Disk, 3-1/2 inch
:
:      COMPUTER: IBM PC compatible
:
:      OPERATING SYSTEM: MS DOS
:
:      SOFTWARE: Wordperfect 5.1
:
:      CURRENT APPLICATION DATA:
:
:      APPLICATION NUMBER: US/08/655,352

```

1 FILING DATE: 800
2 CLASSIFICATION: 800
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: 08/323,449
5 FILING DATE: October 14, 1994
6 ATTORNEY/AGENT INFORMATION:

NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-45000
TELECOMMUNICATION INFORMATION:

TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 nt

LENGTH: 100 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Part of membrane

DESCRIPTION: region of Drosophila Irrequeum (Gen2:Drofreg) with homology to Ily
DESCRIPTION: CCAMK
US-08-655-352-8

Query Match

Best Local Similarity 25.48; Pred. No. 1.2e-11;
Matches 50; Conservative 40; Mismatches 85; Indels 22; Gaps 55;

QY 1 MGGSGSRKSEKELLA EYODLTFTLLTKQEI LLAHRRFCCELLPQEQR TVESSLR AQVPFEQLIS 60
|| | : : : | : : : | : : : |
Db 1 MGKKSSKLQDITDR LTTDTTYFTEKEIR OWHKGFLPKDCPNGLL TEOGFIKIYKOF----- 55

1 MGKSSSKLKQDTIDRLTTDTYETEKEIRQWHKGF LKDCPNGLLTEQGF IKIYKQF----- 55

QY	61	LPELKANDEPERICRVSTSPAKDLSFEDFLDLSVFSDTATPDIKSHYAFRIEDED	120
		: : : : : : : : : : : : : : :	
Db	56	FPQGDPSKFXASLVFRVFDEN-NDGSIIEFEFIRALSVTSRGL--DEKLQWAFRLYDVND	112
QY	121	GTUNREDSLRLVNCL-----TGEGEDTRLASASEMKOLIDNILEESDIDRGTINLSE	172
		: : : : : : : : : : : : : : :	
Db	113	GYTFREEMYNIVDAIYQWGOPOSEDENT-----PQKRVDKIFDQMDKNHDKILTEE	166
QY	173	FGHYISRSPDFASSFKI	189
		: : : : : : : : : : : : : : : : : : : :	
Db	167	FREGSKADPRIVQALSL	183

RESULT 9
US-09-258-016-8
; Sequence 8, Application US/09258016
; Patent No. 6362395

GENERAL INFORMATION:
APPLICANT: Bachettlira W. Poovalah, Zhilua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarkquist Sparkman Campbell Leigh &
ADDRESSEE: Winston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland.
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,016
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stephens Jr., Donald L.
REGISTRATION NUMBER: 34,022
REFERENCE/DOCKET NUMBER: 4630-51994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Region of Drosophila frequen
DESCRIPTION: (Gen2:Drofreg) with homology to Ily
DESCRIPTION: CCAMK

Query Match	18.3%	Score 176;	DB 4;	Length 186;
Best Local Similarity	25.4%;	Pred. No. 1.2e-11;		
Matches 50;	Conservative 40;	Mismatches 85;	Indels 22;	Gaps 5;

```
QY      1 MGGSGSRSLKELLAEYODLTELTTKOEILAHRRCELLPQEORTVESSLRAOVPFEQILS    60
        || :| :| :| | :| :|| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     1 MGAKSSKLQDITDRLLTTDTTYETKEIRQWHKGFLKDPCNGILLTGEQFIKITKYGF-----   55

QY      61 LPELKANPFKERICRVFSTSPAKDSLSEDFELDLLSVFSDTATPDIKSHVAFRIEDEDDEDD    120
        |: :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     56 FPGGDPSKFASLVFRVDEN-NDGSIIEEFIRALSVTSKGL--DEKLQNARFLDYDVND    112
```

```
OY      121 GLNREDLSRLVNC-----TGEEDTRLASASEMKOLIDNILEESDIDRGTINLSE    172  
         | : ||:: .||: :           |:||          ::| |:| :||:| :||  
DB      113 GYTREEMYNIVDAIYQMWGQQPQSEDNT-----PQRVDKIFPDQMKNHDKLTLEE    166  
  
OY      173 FQHVISRSPDFASSFKI    189  
         | : |                : :  
DB      167 FRFGSKADPRIVQALSL    183
```

RESULT 10
US-09-357

```

: Sequence 8, Application US/09257825B
: Patent No. 6403352
: GENERAL INFORMATION:
: APPLICANT: Poovalah, Bachettira W.
: APPLICANT: Patil, Shameekumar
: APPLICANT: Takezawa, Daisuke
: TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plant
: FILE REFERENCE: 4630-51993
: CURRENT APPLICATION NUMBER: US/09/257,825B
: CURRENT FILING DATE: 1999-02-25
: PRIOR APPLICATION NUMBER: US 08/655,352
: PRIOR FILING DATE: 1996-05-23
: PRIOR APPLICATION NUMBER: US 60/014,743
: PRIOR FILING DATE: 1996-03-28
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 8
: LENGTH: 186
: TYPE: PRT
: ORGANISM: Drosophila
US-09-257-825B-8

```

Query Match	18.38;	Score 176;	DB 4;	Length 186;
Best Local Similarity	25.48;	Pred. No. 1.2e-11;		
Matches 50; Conservative	40;	Mismatches 85;	Indels 22;	Gaps 5.

[illegible]

RESULT 11

US-08-764-563-4
Sequence 4, Application US/08764563
Patent No. 6093565
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,449
FILING DATE: October 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-45000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Region of rat neural visinin-like protein
DESCRIPTION: (Gen2:Ratnvp3) with homology to 11ly
DESCRIPTION: CCAMK
US-08-655-352-3

Query Match 15.6%; Score 150; DB 3; Length 193;
Best Local Similarity 24.5%; Pred. No. 9.3e-09;
Matches 51; Conservative 42; Mismatches 79; Indels 36; Gaps 7;

QY 1 MGGSGSRLSKELLAAYODLFTLTKQEILLAHRRFCCLLPQORTVSSSLRAQVPEQILS 60
DB 1 MGKQNSKLREPEVLQDLREHTEFTDHELQEWYKGLKDCPTGHLTVDE-----FKKIYA 53

QY 61 --LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFD 118
DB 54 NFFPYGDASKFAEHVFTFDIN-SDGTIDFREFFIALSVTS-RGKLEQIKWAFSMYDLD 111

QY 119 DDGTLNREDLSRLVNCLTGEGEDTRLASASEM-----QLIDNILESDIDRDGTIN 169
DB 112 GNGYISRSEMLEIVQAI-----YKMVSSVMKMPEDSTPEKRTDKIFROMDINNKGKLS 165

QY 170 LSEF-----QHVISRSPDFASSF 187
DB 166 LEEFIKGAKSDPSIVRLLOCDPSSASQF 193

RESULT 14
US-09-258-016-3
Sequence 3, Application US/09258016
Patent No. 6362395
GENERAL INFORMATION:
APPLICANT: Bachettira W. Poovalah, Zhinhua Liu,
APPLICANT: Shameekumar Patil, Datsuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kiarquist Sparkman Campbell Leigh &
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible.
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,016
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stephens Jr., Donald L.

REGISTRATION NUMBER: 34,022
REFERENCE/DOCKET NUMBER: 4630-51994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Region of rat neural visinin-like protein
DESCRIPTION: (Gen2:Ratnvp3) with homology to 11ly
DESCRIPTION: CCAMK
US-09-258-016-3

Query Match 15.6%; Score 150; DB 4; Length 193;
Best Local Similarity 24.5%; Pred. No. 9.3e-09;
Matches 51; Conservative 42; Mismatches 79; Indels 36; Gaps 7;

QY 1 MGGSGSRLSKELLAAYODLFTLTKQEILLAHRRFCCLLPQORTVSSSLRAQVPEQILS 60
DB 1 MGKQNSKLREPEVLQDLREHTEFTDHELQEWYKGLKDCPTGHLTVDE-----FKKIYA 53

QY 61 --LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFD 118
DB 54 NFFPYGDASKFAEHVFTFDIN-SDGTIDFREFFIALSVTS-RGKLEQIKWAFSMYDLD 111

QY 119 DDGTLNREDLSRLVNCLTGEGEDTRLASASEM-----QLIDNILESDIDRDGTIN 169
DB 112 GNGYISRSEMLEIVQAI-----YKMVSSVMKMPEDSTPEKRTDKIFROMDINNKGKLS 165

QY 170 LSEF-----QHVISRSPDFASSF 187
DB 166 LEEFIKGAKSDPSIVRLLOCDPSSASQF 193

RESULT 15
US-09-257-825B-3
Sequence 3, Application US/09257825B
Patent No. 6403352
GENERAL INFORMATION:
APPLICANT: Poovalah, Bachettira W.
APPLICANT: Patil, Shameekumar
APPLICANT: Takezawa, Datsuke
TITLE OF INVENTION: Compositions and Methods for Production of Male-sterile Plan
FILE REFERENCE: 4630-51993
CURRENT APPLICATION NUMBER: US/09/257,825B
PRIOR FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: US 08/655,352
PRIOR FILING DATE: 1996-05-23
PRIOR APPLICATION NUMBER: US 60/014,743
PRIOR FILING DATE: 1996-03-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 193
TYPE: PRT
ORGANISM: Rat
US-09-257-825B-3

Query Match 15.6%; Score 150; DB 4; Length 193;
Best Local Similarity 24.5%; Pred. No. 9.3e-09;
Matches 51; Conservative 42; Mismatches 79; Indels 36; Gaps 7;

QY 1 MGGSGSRLSKELLAAYODLFTLTKQEILLAHRRFCCLLPQORTVSSSLRAQVPEQILS 60
DB 1 MGKQNSKLREPEVLQDLREHTEFTDHELQEWYKGLKDCPTGHLTVDE-----FKKIYA 53

QY 61 --LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFD 118
DB 54 NFFPYGDASKFAEHVFTFDIN-SDGTIDFREFFIALSVTS-RGKLEQIKWAFSMYDLD 111

Thu Nov 21 18:12:51 2002

us-09-878-454a-2.rai

Page 8

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QY   119 DDGTLNREDSRLVNCLTGEGETRSLASEMK-----QLIDNILEESDIDRGCTIN 169  
      :|::|| :: | | :: || | | : | | : || :  
Db    112 GNGYSIRSEMLEIVOA I ----- YKVVSVMMKPPEDESTPERKTDKIFROMINDNGKIS 165  
  
QY    170 LSEF-----QHVISRSPPDFASSF 187  
      | |       :: | | | |  
Db     166 LEEFIKAKS DPSI VRLLQC DPSSAS Q F 193
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Search completed: November 21, 2002, 17:59:54
Job time : 16 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2002, 17:58:20 ; Search time 11 Seconds

(without alignments)
271.941 Million cell updates/sec

Title: US-09-878-454A-2

Perfect score: 962

Sequence: 1 MGGSGSRSLKELLAEYQDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100480 segs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	962	100.0	191	10	US-09-878-454A-2
2	950	98.8	191	12	US-10-109-885-2
3	345	35.9	187	10	US-09-802-116-2
4	186.5	19.4	170	12	US-10-109-885-3
5	179.5	18.7	195	10	US-09-999-602-3
6	174.5	18.1	195	10	US-09-999-602-4
7	146	15.2	220	10	US-09-350-874-26
8	141	14.7	220	10	US-09-350-874-24
9	141	14.7	220	10	US-09-350-874-20
10	141	14.7	220	10	US-09-350-874-14
11	138	14.3	216	10	US-09-350-874-6
12	138	14.3	227	10	US-09-350-874-8
13	138	14.3	227	10	US-09-350-874-10
14	138	14.3	245	10	US-09-350-874-4
15	138	14.3	270	10	US-09-350-874-18
16	137	14.2	216	10	US-09-350-874-2
17	136.5	14.2	214	10	US-09-999-602-1
18	136	14.1	225	10	US-09-350-874-30
19	136	14.1	252	10	US-09-350-874-22

20	136	14.1	252	10	US-09-350-874-28	Sequence 28, Appl
21	136	14.1	252	10	US-09-350-874-42	Sequence 42, Appl
22	136	14.1	257	10	US-09-350-874-16	Sequence 16, Appl
23	126	13.1	229	10	US-09-350-874-70	Sequence 70, Appl
24	126	13.1	233	10	US-09-350-874-49	Sequence 49, Appl
25	126	13.1	250	10	US-09-350-874-72	Sequence 72, Appl
26	113.5	11.8	1210	10	US-09-922-217-692	Sequence 692, App
27	113.5	11.8	1210	10	US-09-833-263-692	Sequence 692, App
28	113.5	11.8	1548	10	US-09-922-217-1095	Sequence 1095, Ap
29	112.5	11.7	172	12	US-10-109-885-4	Sequence 4, Appl
30	112	11.6	256	10	US-09-350-874-32	Sequence 32, Appl
31	111.5	11.6	142	10	US-09-910-071-4	Sequence 4, Appl
32	110	11.4	203	10	US-09-350-874-12	Sequence 12, Appl
33	110	11.4	652	9	US-09-554-000-2	Sequence 2, Appl
34	110	11.4	652	9	US-09-554-000-4	Sequence 4, Appl
35	109	11.3	256	10	US-09-350-874-36	Sequence 36, Appl
36	108	11.2	642	9	US-09-554-000-6	Sequence 6, Appl
37	108	11.2	656	9	US-09-554-000-8	Sequence 8, Appl
38	107.5	11.2	159	10	US-09-910-071-5	Sequence 5, Appl
39	107.5	11.2	201	10	US-09-925-297-714	Sequence 714, App
40	102.5	10.7	139	10	US-09-864-761-34808	Sequence 34808, A
41	95.5	9.9	90	10	US-09-826-589-3	Sequence 3, Appl
42	95.5	9.9	90	10	US-09-826-589-4	Sequence 4, Appl
43	95.5	9.9	90	10	US-09-872-1858-11	Sequence 11, Appl
44	95.5	9.9	90	10	US-09-872-1858-12	Sequence 12, Appl
45	95	9.9	1604	10	US-09-888-615-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1

US-09-878-454A-2

Sequence 2, Application US/09878454A

Patent No. US20020064828A1

GENERAL INFORMATION:

APPLICANT: Monteliro, et al.

TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentin

FILE REFERENCE: 4115-161

CURRENT APPLICATION NUMBER: US/09/878,454A

CURRENT FILING DATE: 2001-06-11

PRIOR APPLICATION NUMBER: 60/210,939

PRIOR FILING DATE: 2000-06-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 191

TYPE: PRT

ORGANISM: Homo sapiens

US-09-878-454A-2

Query Match 100.0%; Score 962; DB 10; Length 191;

Best Local Similarity 100.0%; Pred. No. 2.3e-89;

Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGSGSRSLKELLAEYQDLTFLTKQELIAHRRFCELLPOEORTVESSLRACVPFEQILS 60

DB 1 MGGSGSRSLKELLAEYQDLTFLTKQELIAHRRFCELLPOEORTVESSLRACVPFEQILS 60

QY 61 LPELKANPFRKICRVFSTSPAKDSLFEDELIDLSVSFSDTATPDIKSHYAFRIFDQDD 120

DB 61 LPELKANPFRKICRVFSTSPAKDSLFEDELIDLSVSFSDTATPDIKSHYAFRIFDQDD 120

QY 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRDGTLNLESEFQHVISR 180

DB 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRDGTLNLESEFQHVISR 180

QY 181 PDFASSFKIVL 191

DB 181 PDFASSFKIVL 191

RESULT 2

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US-10-109-885-2
; Sequence 2, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND METH
; TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON
; FILE REFERENCE: REVEL-14A
; CURRENT APPLICATION NUMBER: US/10/109,885
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 6b/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-109-885-2

```

```

Query Match          98.8%; Score 950; DB 12; Length 191;
Best Local Similarity 99.0%; Pred. No. 3.7e-88;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MGGSGSRLSKELLAAYODLFTLKQELLAAHRRCELLPQEQRTVESSLAQVPEQILS 60
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DB 1 MGGSGSRLSKELLAAYODLFTLKQELLAAHRRCELLPQEQRTVESSLAQVPEQILS 60
QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEFLLDLSVFSDTATPDIKSHYAFRIFFDDDD 120
    |||||
DB 61 LPELKANPFKERICRVFSTSPAKDSLSFEFLLDLSVFSDTATPDIKSHYAFRIFFDDDD 120
QY 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQHVISRS 180
    |||||
DB 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQHVISRS 180
QY 181 PDFASSFKIYL 191
    |||||
DB 181 PDFASSFKIYL 191

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RESULT 3
US-09-802-116-2
; Sequence 2, Application US/09802116
; Patent No. US20020082406A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020082406A1 Human Kinase Interacting Protein and Polynu
; TITLE OF INVENTION: the Same
; FILE REFERENCE: LEX-0146-USA
; CURRENT APPLICATION NUMBER: US/09/802,116
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/187,719
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 187
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-802-116-2

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Query Match          35.9%; Score 345; DB 10; Length 187;
Best Local Similarity 40.4%; Pred. No. 1.6e-27;
Matches 78; Conservative 42; Mismatches 61; Indels 12; Gaps 5;

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QY 1 MGGSGSRLSKELLAAYODLFTLKQELLAAHRRCELLPQ---EQRTVESSLAQVPE 56
    || : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MGNKQTVFTHEQLAYQDCTFFTRKEIMRLFYRYQDLAPQLVPLDYTTCPD---VKVPYE 57
QY 57 QILSLPELKANPFKERICRVFSTSPAKDSLSFEFLLDLSVFSDTATPDIKSHYAFRIED 116
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 58 LIGSMPELKDNPFQRIQAVFS-EDGDGHMTLDNFDMSVSMSEMAPRDLKAYYAFKIYD 116
QY 117 FDDGTNLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQHV 176
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 117 FNNDYICAMDEQVTKLT-RGE---LSAEVSLVCEKVLDEADGDHGRSLSEDFQNM 172
QY 177 ISRSPDFASSEKI 189
    | : | | | | | | |
DB 173 ILRAPDFLSTFHT 185

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RESULT 4
US-10-109-885-3
; Sequence 3, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND
; FILE REFERENCE: REVEL-14A
; CURRENT APPLICATION NUMBER: US/10/109,885
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-109-885-3

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Query Match          19.4%; Score 186.5; DB 12; Length 170;
Best Local Similarity 31.1%; Pred. No. 1.1e-11;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;

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QY 56 EQILSLPELKANPFKERICRVFSTSPAKDSLSFEFLLDLSVFSDTATPDIKSHYAFRIE 115
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 41 EEFMSLPQLQNPVQVRVIDFTD-GNGEVDERKEFIEGVQSQSVKGDKQKIRAFRIY 99
QY 116 DEDDGTNLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQHV 175
    | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
DB 100 DMDKDGYSISNGELFQVLKMAVG---NNLKDTQLQOIIVDKTINADKDGGRISFEFCA 155
QY 176 VI 177
    | :
DB 156 VV 157

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RESULT 5
US-09-999-602-3
; Sequence 3, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON

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: CURRENT APPLICATION NUMBER: US/09/999,602
: CURRENT FILING DATE: 2001-10-25
: PRIOR APPLICATION NUMBER: 09/010,378
: PRIOR FILING DATE: 1998-01-21
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PERL Program
: SEQ ID NO 3
: LENGTH: 195
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No. US20020091084A1 g1226242
US-09-999-602-3

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Query Match	18.7%	Score 179.5;	DB 10;	length 195;
Best Local Similarity	26.7%;	Pred. No. 6.5e-11;		
Matches 52; Conservative	36;	Mismatches 78;	Indels 29;	Gaps 6;

[illegible]

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RESULT 6
US-09-999-602-4
; Sequence 4, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Nell C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON
; CURRENT APPLICATION NUMBER: US/09/999,602
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/010,378
; PRIOR FILING DATE: 1998-01-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020091084A1 91706967
US-09-999-602-4

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Query Match          18.18; Score 174.5; DB 10; Length 195;
Best Local Similarity 26.28; Pred. No. 2.1e-10;
Matches 51; Conservative 36; Mismatches 79; Indels 29; Gaps 6;

QY 1 MGGSGSRLSK-ELLAEXODTFLTKOEILLAHRRFCCLLPQEQRTVESSLRAQVPEQIL 59
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MGSRASTLLRDEELLEIRKETGFSSHQITRLYSRFTSLDKGNGTLSR-----EDFQ 52

QY 60 SLPELKANPFKERICRYVESTSPAKDSLSFEDFLDLVSF-----SDTATPD----- 105
   :||| | | :|| | | | | | | | | | | | | | | | | | | | | |
Db 53 RIPELAINPLGDRILNAFPE-GEDQVNRGEFMRTLAHRRPIEDNEKSKDVNGPEPLNSR 111

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[illegible]

RESULT 7
US-09-35

US-09-350-874-26
; Sequence 26, Application US/09350874
; Patent No. US20090100001

```

; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Simlan sp.
US-09-350-874-26

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Query Match.	15.2%;	Score 146;	DB 10;	Length 220;
Best Local Similarity	23.9%;	Pred. No. 1.8e-07;		
Matches 44;	Conservative 45;	Mismatches 81;	Indels 14;	Gaps 5;

```
QY      11 ELLAEYODLTFLTKOEILLAHRRFCCELLPQEQRVTESSSLRAQVPFEQILS--LPPELKANP   68
        | : | : | : : : : : | : : | : | : | : : :
Db      41 EGLEQLQEQCTKTRKELQVLRYRGFKNECP-----SGIVNEENFKQIYSQFFPOGDSST   93
        | : | : | : : : : : | : : | : | : | : : :
QY      69 FKERICRVESTSPAKDLSFEDFLDLLSVESDTPATPDIKSHYAFRIFDFDDDGITLRNRE--  126
        : : : : | : : : : | : | : | : | : | : : : :
Db      94 YAFLENAFDTN-HDGSVSFEDEFVAGLSYL-RGTVDRLNMAFNLYDLNKDCGITKEEM    151
        : : : : | : : | : | : | : | : | : | : : : :
QY     127 -DLSRLVNCLTGEGEDTRLASASEMKOLIDNILLESDIDRDGTINLSEFOHVISRSPDEAS  185
        | : : : : | : : : : | : : : : | : : : : | : : : :
Db     152 LDIMKSIIYDMMGKYTYPALRREAPREHVENFFQKMDRNKGDVVTIEEFIESCQKDENIMR    211
        | : : : : | : : : : | : : : : | : : : : | : : : :
QY     186 SFKI 189
        | : : : : | : : : : | : : : : | : : : : | : : : :
Db     212 SMOJ 215
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RESULT 8
US-09-35

US-09-350-874-24
; Sequence 24, Application US/09350874

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; GENERAL INFORMATION:
;
; APPLICANT: Rhodes, Kenneth
;
; TITLE OF INVENTION: METHOD
;
; FILE REFERENCE: MNI-069
;
; CURRENT APPLICATION NUMBER: US/09/350,874
;
; CURRENT FILING DATE: 1999-07-09
;
; EARLIER APPLICATION NUMBER: USSN 60/110,277
;
; EARLIER FILING DATE: 1998-11-30
;
; EARLIER APPLICATION NUMBER: USSN 60/110,033
;
; EARLIER FILING DATE: 1998-11-25
;
; EARLIER APPLICATION NUMBER: USSN 60/109,333
;

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Db      66  EGLEQLAQTNETFKRELQVLYRGFKNECP-----SGVNEETFKQIYAQFFPHGDAST 118
QY      69  FKERICRVSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIEDDDGTINREDL 128
Db      119  YAHYLENAFDITQT-GSVKFEDEFTALSTLL-RGTVHEKLRWTFNLIDINKDGYINKEEM 176
QY      129  SRLVNC--LNGEGDTRLASASEMKOLIDNILESDIDRDGTINLSEF 173
Db      177  MDIVKAIYDMGKYYTPVLKEDTPRQHVDFVFOKMDKNKDGIYTLDEF 224

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RESULT 15

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US-09-350-874-18
; Sequence 18, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-350-874-18

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Query Match 14.3%; Score 138; DB 10; Length 270;
 Best Local Similarity 25.0%; Pred. No. 1.5e-06;
 Matches 42; Conservative 42; Mismatches 70; Indels 14; Gaps 5;

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QY      69  FKERICRVSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIEDDDGTINREDL 126
Db      144  YAHYLENAFDITN-HDGSVSFEDFVAGLSVIL-RGTIDRLNWAFFNLIDLKDGCTKKEEM 201
QY      127  -DLSRLVNCITGEGEDTRLASASEMKOLIDNILESDIDRDGTINLSEF 173
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Search completed: November 21, 2002, 18:00:35
 Job time : 12 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 21, 2002, 17:57:51 ; Search time 35 Seconds

(without alignments)
727.168 Million cell updates/sec

Title: US-09-878-454A-2

Perfect score: 962

Sequence: 1 MGGSGSRSLSKELLAAYQDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : A_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	958	99.6	191	19 AAW51215	Amino acid sequence
2	952	99.0	191	19 AAW62287	Human protein phos
3	950	98.8	191	19 AAW64199	Human interferon r
4	379	39.4	172	22 AAU87324	Human central nerv
5	379	39.4	184	22 AAW43562	Human polypeptide
6	377	39.2	185	22 AAB64418	Amino acid sequenc
7	362	37.6	173	22 ABB96054	Human testicular a
8	362	37.6	173	22 AAU87612	Novel central nerv
9	362	37.6	173	22 AAW95362	Human reproductive
10	362	37.6	173	22 AAW43637	Human polypeptide

11	362	37.6	173	22 AAU19952	Novel human calciu
12	345	35.9	187	22 AAE09736	Human kinase inter
13	343.5	35.7	206	22 ABB64325	Drosophila melanog
14	244.5	25.4	169	23 ABP41194	Human ovarian anti
15	220	22.9	120	20 AAY11976	Human 5' EST secre
16	204.5	21.3	175	20 AAY00881	Calcineurin regula
17	195	20.3	175	21 AAG21178	zeae may protein f
18	195	20.3	210	21 AAG21177	zeae may protein f
19	194	20.2	175	21 AAG51586	Arabidopsis thalia
20	194	20.2	175	23 ABB92357	Herbicidally activ
21	192	20.0	175	21 AAG07824	Arabidopsis thalia
22	186.5	19.4	170	19 AAW64200	Human calcineurin.
23	186.5	19.4	170	21 AAB09978	Human HCNB protein
24	185	19.2	169	21 AAG51587	Arabidopsis thalia
25	183	19.0	169	21 AAG07825	Arabidopsis thalia
26	182.5	19.0	189	22 ABB58936	Drosophila melanog
27	181	18.8	169	21 AAG21179	zeae may protein f
28	176.5	18.3	187	22 ABB61857	Drosophila melanog
29	176.5	18.3	187	22 ABB67063	Drosophila melanog
30	175.5	18.2	162	22 ABB65554	Drosophila melanog
31	174.5	18.1	170	22 ABB60493	Drosophila melanog
32	170	17.7	170	21 AAB09977	Human CNBIR protei
33	170	17.7	173	22 AAO14411	Calcineurin B subu
34	170	17.7	173	22 AAB64410	Amino acid sequenc
35	170	17.7	187	22 AAU87327	Novel central nerv
36	170	17.7	189	22 ABB95936	Human testicular a
37	170	17.7	189	22 AAU87615	Novel central nerv
38	170	17.7	189	22 AAM95239	Human reproductive
39	170	17.7	189	22 AAM43564	Human polypeptide
40	170	17.7	189	22 AAM43639	Human polypeptide
41	170	17.7	189	22 AAU19951	Novel human calciu
42	164.5	17.1	226	21 AAG47032	Arabidopsis thalia
43	163.5	17.0	226	21 AAG21763	Arabidopsis thalia
44	157	16.3	190	21 AAY69996	Human receptor-ass
45	156	16.2	194	22 AAU87585	Novel central nerv

ALIGNMENTS

RESULT 1
AAW51215
ID AAW51215 standard; Protein; 191 AA.

AAW51215;
21-AUG-1998 (first entry)

Amino acid sequence of the calcium-integrin binding protein.
Human calcium-integrin binding protein; CIB; integrin alpha IIB;
cytoplasmic domain; platelet; alpha IIB-beta-3; fibrinogen receptor;
inhibition; blood coagulation; vascular disorder.

Homo sapiens.

Key	Location/Qualifiers
Region	116..128
Region	/note="EF-hand motif"
Region	160..173
Region	/note="EF-hand motif"

PN	W09814471-A1.
XX	
PD	09-APR-1998.
XX	
PF	24-SEP-1997; 97WO-US16828.
XX	
PR	02-OCT-1996; 96US-0720625.
XX	
PA	(UINC-) UNIV NORTH CAROLINA.
XX	
PI	Naik UP, Parise LV;

XX WPI; 1998-240018/21.
DR N-PSDB; AAV07211.
XX
PT New isolated calcium-integrin binding protein - is expressed in
PT platelets and activates the fibrinogen receptor, used to develop
PT products for treating e.g. vascular disorders
XX
PS Claim 1; Page 30; 44pp; English.
XX
CC This is the amino acid sequence of the human calcium-integrin binding
CC (CIB) protein, that binds to the integrin alpha IIB cytoplasmic
CC domain. The CIB protein is expressed in platelets and interacts with
CC the alpha IIB subunit of integrin alpha IIB-beta 3, to activate the
CC fibrinogen receptor. Inhibitory compounds can be used to inhibit the
CC activation of the fibrinogen receptor where it is desired to reduce
CC blood coagulation for therapeutic, diagnostic or pharmaceutical
CC reasons. The products can be used for treating vascular disorders,
CC and for isolating or purifying integrins or fibrinogen. They can also
CC be used for detection and diagnosis.
XX
SQ Sequence 191 AA;

Query Match 99.6%; Score 958; DB 19; Length 191;
Best Local Similarity 99.5%; Pred. No. 3.3e-93;
Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGGSGSRLSKELLAAYQDLFTLKQELLAAHRRFCCELLPQEQRTVESSLRAQVPFEQILS 60
DB 1 MGGSGSRLSKELLAAYQDLFTLKQELLAAHRRFCCELLPQEQRTVESSLRAQVPFEQILS 60
OY 61 LPELKANPKEKRICRVSTSPAKDSLSEFEDLVLVSFSDTATPDIKSHYAFRIEDFDD 120
DB 61 LPELKANPKEKRICRVSTSPAKDSLSEFEDLVLVSFSDTATPDIKSHYAFRIEDFDD 120
OY 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNLEESDIDRDGTINLSEFQHVISR 180
DB 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNLEESDIDRDGTINLSEFQHVISR 180
OY 181 PDFASSFKIVL 191
DB 181 PDFASSFKIVL 191

RESULT 2

AAW62287
ID AAW62287 standard; Protein; 191 AA.

XX AAW62287;

DT 24-SEP-1998 (first entry)

DE Human protein phosphatase regulatory subunit.

KW Human; protein phosphatase regulatory subunit; HCNB; diagnosis;
KW immunosuppression; neurodegeneration; inflammation; cancer.

OS Homo sapiens.

FT Key Location/Qualifiers
FT Misc-difference 44 /label= unknown
FT /note= "encoded by ASG"
FT Misc-difference 45 /label= unknown
FT /note= "encoded by TGN"

PN WO9826056-A1.

PD 18-JUN-1998.

PF 25-NOV-1997; 97WO-US21603.

XX

PR 12-DEC-1996; 96US-0764563.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Goli SK, Hillman JL;
XX
DR WPI; 1998-348518/30.
DR N-PSDB; V398009.
XX
PT New protein phosphatase regulatory sub-unit - useful for diagnosis,
PT prevention and treatment of immuno-suppression, neuro-degeneration,
PT inflammation and cancer
XX
PS Claim 1; Fig 1; 65pp; English.

XX The present sequence is a pure human protein phosphatase regulatory
CC subunit (HCNB). Host cells, comprising a vector containing DNA encoding
CC HCNB, are used to produce recombinant HCNB which is used to treat or
CC prevent immunosuppression or neurological diseases (especially parasitic,
CC bacterial or viral infections, including AIDS; the effects of radio- or
CC chemo-therapy and Alzheimer's disease). Antagonists which bind
CC specifically to HCNB and modulate its activity are used to treat
CC inflammation, cancer, or immunological disorders and allograft rejection
CC (especially anaemia, asthma, systemic lupus erythematosus, myasthenia
CC gravis, diabetes, thyroiditis, ulcerative colitis, osteoporosis and
CC arthritis). Complements of the DNA encoding HCNB are useful as probes
CC and primers for detecting the DNA encoding HCNB by hybridisation or
CC amplification assays, while Ab can be used to detect HCNB by immunoassay,
CC particularly for diagnosis of the specified disorders, including early
CC diagnosis of cancers. The probes can also be used to map the
CC corresponding genomic sequence, while Ab are also useful in drug
CC screening and for purifying native HCNB. Therapeutic agents are
CC administered orally, intravenously, intramuscularly, topically or
CC rectally, normally at 0.1-105 mg.

SQ Sequence 191 AA;
Query Match 99.0%; Score 952; DB 19; Length 191;
Best Local Similarity 99.0%; Pred. No. 1.4e-92;
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 MGGSGSRLSKELLAAYQDLFTLKQELLAAHRRFCCELLPQEQRTVESSLRAQVPFEQILS 60
OY 61 LPELKANPKEKRICRVSTSPAKDSLSEFEDLVLVSFSDTATPDIKSHYAFRIEDFDD 120
DB 61 LPELKANPKEKRICRVSTSPAKDSLSEFEDLVLVSFSDTATPDIKSHYAFRIEDFDD 120
OY 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNLEESDIDRDGTINLSEFQHVISR 180
DB 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNLEESDIDRDGTINLSEFQHVISR 180
OY 181 PDFASSFKIVL 191
DB 181 PDFASSFKIVL 191

RESULT 3

AAW64199
ID AAW64199 standard; Protein; 191 AA.

XX AAW64199;

DT 09-NOV-1998 (first entry)

DE Human interferon receptor 1 binding protein IR1B1.

KW Interferon receptor 1 binding protein; IR1B1; human; tumour;
KW cancer; gene therapy; tissue graft; graft survival.

OS Homo sapiens.

XX

PN WO9831796-A1.
XX
XX 23-JUL-1998.
PD
XX 15-JAN-1998; 98WO-US00671.
XX
XX 15-JAN-1997; 97US-0035636.
PR
XX (MCIN/) MCINNIS P A.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Abramovitch C, Chebath JE, Revel M;
XX
XX WPI; 1998-414096/35.
DR
DR N-PSDB; AAV44272.
XX
PT New isolated interferon receptor binding proteins - used to develop
PT products for modulating sensitivity to interferon, e.g. in the
PT treatment of tumours or for prolonging graft survival
XX
XX
PS Claim 1; Page 34; 64pp; English.

CC This is a novel human protein, designated interferon receptor
CC binding protein 1 (IRIB1), which interacts with the intracytoplasmic
CC (IC) domain of the IFNAR1 chain of the interferon type I (IFN-alpha,
CC beta or omega) receptor. IRIB1 is a new member of the calcineurin
CC and calcitracin family of calcium-regulated proteins (see also
CC AAW64200). It is induced very rapidly and transiently following IFN
CC treatment of human cells. It was identified in a two-hybrid
CC screening for proteins interacting with the IFNAR1-IC domain;
CC another protein, IRIB4 (see AAW64202), was similarly identified. A
CC cDNA clone (see AAV44272) encoding IRIB1, host cells and expression
CC vectors are claimed. DNA encoding IRIB1 and IRIB4 can be used in
CC cancer therapy where the increased cellular response to IFN would
CC result in a decrease in malignant cell growth and an enhanced
CC response to exogenous IFN therapy. Antisense IRIB1 or IRIB4
CC nucleic acids can be used for prolonging tissue or organ graft
CC survival in patients as the rejection of these grafts in the host
CC is mediated by the histocompatibility antigens (MHC class I) whose
CC synthesis depends on the IFN stimulus. The products can also be
CC used in detection and diagnosis.

XX
SQ Sequence 191 AA;

Query Match 98.8%; Score 950; DB 19; Length 191;
Best Local Similarity 99.0%; Pred. No. 2.3e-92;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MGSGSRLSKELLAAYQDLTFLTKQELLAHRRFCCELLPOEORSVSSLRAQVPEEQILS 60
OY 61 LPELKANPFRERICRVFSTSPAKDSLSFEDELIDLSVFSDTATPDIKSHYAFRIFFDDDD 120
Db 61 LPELKANPFRERICRVFSTSPAKDSLSFEDELIDLSVFSDTATPDIKSHYAFRIFFDDDD 120
OY 121 GTLNREDLSRLVNCITGEGEDTRLSASEMKQOLIDNILESDIDRDGTINLSEFOHVISRS 180
Db 121 GTLNREDLSRLVNCITGEGEDTRLSASEMKQOLIDNILESDIDRDGTINLSEFOHVISRS 180
OY 181 PDFASSFRIVL 191
Db 181 PDFASSFRIVL 191

RESULT 4
AAU87324
ID AAU87324 standard; Protein; 172 AA.
XX
XX AAU87324;
XX
XX 05-JUN-2002 (first entry)
DE
XX

DE Novel central nervous system protein #234.
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX
XX Homo sapiens.
OS
XX
XX WO200155318-A2.
PN
XX
PD 02-AUG-2001.
XX
XX
PF 17-JAN-2001; 2001WO-US01332.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 11-JUL-2000; 2000US-0217487.
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PR 14-JUL-2000; 2000US-0218290.
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PR 14-AUG-2000; 2000US-0224518.
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PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
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PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 05-SEP-2000; 2000US-0229509.
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PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
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PR 12-SEP-2000; 2000US-0231968.

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PR	14-SEP-2000;	2000US-0232399.
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PR	02-OCT-2000;	2000US-0237037.
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PR	02-OCT-2000;	2000US-0237039.
PR	02-OCT-2000;	2000US-0237040.
PR	13-OCT-2000;	2000US-0239937.
PR	13-OCT-2000;	2000US-0239937.
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PR	20-OCT-2000;	2000US-0241121.
PR	20-OCT-2000;	2000US-0241786.
PR	20-OCT-2000;	2000US-0241787.
PR	20-OCT-2000;	2000US-0241808.
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PR	20-OCT-2000;	2000US-0241826.
PR	01-NOV-2000;	2000US-0244617.
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PR	17-NOV-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250160.
PR	01-DEC-2000;	2000US-0250391.

PR 05-DEC-2000; 2000US-0251030.
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 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
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 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI; 2001-581633/65.
 DR N-PSDB; ABK43654.
 DR
 XX
 XX
 PT New isolated nucleic acid encoding a protein for diagnosing,
 PT preventing, treating or ameliorating medical conditions and used as
 PT food additives or preservatives -
 XX
 PS Claim 9; SEQ ID No 842; 837pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (II) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amyotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

Query Match	39.4%;	Score 379;	DB 22;	Length 172;
Best Local Similarity	44.1%;	Pred. No. 5.6e-32;		
Matches 78; Conservative	36;	Mismatches 53;	Indels 10;	Gaps 3

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QY      13 LAEYODTEFLTKOEILLAHRRFCCELLPQEORTVESSLRAQVPFEQILSLPELKANPEKER 72
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 LEEYQALTEVLRNEILCIHDTFLKCPGKYYKEATL----TMDQVSSLPALRVNPFDR 56

QY      73 ICRVFSTSPAKDLSFEDEFLDLLSVFSDTATPDIKSHYAFRIFDDEDDGTLNREDLSRLV 132
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Db      57 ICRVFS--HKGMFSFEDVLGMASVSEQACPSLKIEYAFRIYDFENENGFIDEEDLORII 113

QY      133 NCLTGEGETRLSASEMKOLIDNILEESDIDRGTINLSEFOHVISRSPDFASSFKI 189
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Db      114 LRLNDD--MSEDLMDLTNHLVSESDDLNDNMLSFEEHAMAKSPDEMNSTR 167

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RESULT	5
AAM43562	
ID	AAM43562 standard; Protein; 184 AA
XX	
AC	AAM43562;
XX	
DT	22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 240.
XX KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antiulcer; vulnery; anticonvulsant; antibacterial;
KW antiparasitic; cardiac; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX OS Homo sapiens.
XX PN WO200155308-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01309.
XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
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05-DEC-2000; 2000US-0256719.
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PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-488781/53.
DR N-PSDB; AAI63868.
XX
PT New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating and/or preventing human diseases and disorders -
XX
PS Claim 11; SEQ ID NO 240; 664pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI63803-AAI64012) and
CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 184 AA;
Query Match 39.4%; Score 379; DB 22; Length 184;
Best Local Similarity 44.1%; Pred. No. 6.2e-32;
Matches 78; Conservative 36; Mismatches 53; Indels 10; Gaps 3;
QY 13 LAEYQDLTFLTKQEIILAHRRFCELLPQEQRTVESSLRAQVPFEQILSLPELKANPEK 72
Db 13 LEEYQALFTLRNEILCIHDTFLKCPGKYKEATL-----TMDQVSSLPALRVNPFDR 68
QY 73 ICRVFTSPAKDSLSEFEDLILSVESDTATPDIKSHYAFRIFFDDGTLNREDISRLV 132
Db 69 ICRVFS---HKGMFSFEDVLGMASVFSEQACPSLKIEYAFRIYDENENGFIDEEDIQRII 125
QY 133 NCLTGEEDTRLASASEKQOLIDNILESDIDRDGTINLSEFQHVISRSPDFASSFKI 189
Db 126 LRLINSDD---MSEDLMDLTNHLVLSSEDLNDNMLSEFSEFHAMAKSPDFMNSFRI 179
RESULT 6
AAB64418
ID AAB64418 standard; Protein; 185 AA.
XX
AC AAB64418;
XX
DT 22-MAR-2001 (first entry)
XX
DE Amino acid sequence of human intracellular signalling molecule INTRA50.
XX
KW Human; intracellular signalling molecule; INTRA; immunosuppressive;
KW cytosolic; neuroprotective; nootropic; antiarteriosclerotic; cancer;
KW antiinflammatory; anti-HIV; neuroleptic; antibacterial; antifungal;

anti-viral; antiparasitic; antihelminthic; antiparkinsonian; AIDS;
KW cell proliferative disorder; arteriosclerosis autoimmune; epilepsy;
KW inflammatory disorder; Addison's disease; gastrointestinal disorder;
KW neurological disorder; Parkinson's disease; Creutzfeldt-Jakob disease;
KW mental disorder; schizophrenia; anxiety.
XX
OS Homo sapiens.
XX
PN WO200077040-A2.
XX
PD 21-DEC-2000.
XX
PE 16-JUN-2000; 2000WO-US16636.
XX
PR 16-JUN-1999; 99US-0139566.
PR 17-AUG-1999; 99US-0149640.
PR 09-NOV-1999; 99US-0164417.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yue H, Tang YF, Hillman JL, Lal P, Bandman O, Baughn MR;
PI Azimzai Y, Yang J, Reddy R, Lu DAM;
XX
DR WPI; 2001-025334/03.
DR N-PSDB; AAF32687.
XX
PT New human intracellular signalling molecules, useful for the diagnosis,
PT prevention and treatment of cell proliferative, autoimmune,
PT inflammatory, neurological, gastrointestinal, reproductive and
PT developmental disorders -
XX
PS Claim 5; Page 158-159; 192pp; English.
XX
CC Sequences AAF32638 - AAF32689 represent cDNA encoding human
CC intracellular signalling molecules INTRA1 - INTRA52, represented in
CC AAB64369 - AAB64420. Modulators of the intracellular signalling molecules
CC of the invention exhibit immunosuppressive; cytosolic; neuroprotective;
CC nootropic; antiarteriosclerotic; antiinflammatory; anti-HIV;
CC neuroleptic; antibacterial; antifungal; antiviral; antiparasitic;
CC antihelminthic; and antiparkinsonian activity. INTRA polypeptides their
CC agonists and antagonists are useful for the treatment of a condition
CC associated with decreased or increased expression of functional INTRA.
CC Disorders associated with abnormal INTRA expression or activity include
CC cell proliferative disorders e.g. arteriosclerosis and cancers;
CC autoimmune or inflammatory disorders e.g. Addison's disease and acquired
CC immunodeficiency syndrome (AIDS); viral, bacterial, fungal, parasitic,
CC protozoal and helminthic infections; gastrointestinal disorders e.g.
CC dysphagia and irritable bowel syndrome; neurological disorders e.g.
CC epilepsy and Parkinson's disease; prion diseases e.g. Creutzfeldt-Jakob
CC disease and mental disorders e.g. anxiety, schizophrenia and Tourette's
CC disorder. Antibodies immunospecific for the INTRA proteins may also be
CC useful in the diagnosis of the above disorders.
XX
SQ Sequence 185 AA;
Query Match 39.2%; Score 377; DB 22; Length 185;
Best Local Similarity 44.1%; Pred. No. 1e-31;
Matches 79; Conservative 35; Mismatches 55; Indels 10; Gaps 3;
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Db 12 ELEEYQALFTLRNEILCIHDTFLKCPGKYKEATL-----TMDQVSSLPALRVNPF 67
QY 71 EICRVFTSPAKDSLSEFEDLILSVESDTATPDIKSHYAFRIFFDDGTLNREDISR 130
Db 68 DRICRVFS---HKGMFSFEDVLGMASVFSEQACPSLKIEYAFRIYDENENGFIDEEDLQR 124
QY 131 LVNCLTGEEDTRLASASEKQOLIDNILESDIDRDGTINLSEFQHVISRSPDFASSFKI 189
Db 125 ILRLINSDD---MSEDLMDLTNHLVLSSEDLNDNMLSEFSEFHAMAKSPDFMNSFRI 180
RESULT 7

ABB96054
ID ABB96054 standard; Protein; 173 AA.
XX
AC ABB96054;
XX
DT 21-JUN-2002 (first entry)
XX
DE Human testicular antigen SEQ ID NO: 1438.
XX
KW Human; testicular antigen; testes; cancer; metastasis; immune disorder;
KW reproductive system disorder; urinary system disorder; gene therapy;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disease; infection; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200155317-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01329.
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PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR	13-OCT-2000;	2000US-0239967
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PR	05-DEC-2000;	2000US-0251030
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PR	05-JAN-2001;	2001US-0259678
XX	(HUMA-) HUMAN GENOME SCI INC	

PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-581633/65.
DR N-PSDB; ABK43942.
XX
PT New isolated nucleic acid encoding a protein for diagnosing,
PT preventing, treating or ameliorating medical conditions and used as
PT food additives or preservatives -
XX
PS
XX Claim 9; SEQ ID No 1130; 837pp; English.
CC
CC The invention describes an isolated nucleic acid molecule (I) encoding a
CC novel central nervous system protein. (I) and polypeptides (III) encoded
CC by (I), are used to treat a medical conditions and in diagnosis of a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukaemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infarction. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,

Query Match	37.6%;	Score 362;	DB 22;	Length 173;
Best Local Similarity	42.9%;	Pred. No. 3.6e-30;		
Matches 75; Conservative	35;	Mismatches 55;	Indels 10;	Gaps 3;

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QY 13 LAEYQDLEFLTKOEILLAHRRFCELLPOEORIVESSLRAQVPFEQILSLPELKANPEKER 72
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Db 57 ICRVFS---HKGMFSFEDVLGMASVFSEACPSLKIEYAFRIYDFENENGFIDEEDLQRII 113
QY 133 NCLTGEGEDTRLASASEMKOLIDNILEESDIDRDTGTLNLSFQHVISRSPDFASSF 187
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Db 114 LRLNSDD---MSEDLIMDLTINHVLXSXSDLDNDNMLSFSEFEHAMAKSPDPTPTF 165

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RESULT 9
AAM95362
ID AAM95362 standard; Protein; 173 AA

AC AAM95362;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen SEQ ID NO: 4020.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
XX cancer; gene therapy.
OS Homo sapiens.
XX
PN WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01339.
XX

PR 31-JAN-2000; 2000US-0179065.
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PR 01-DEC-2000; 2000US-0250391.
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PR 08-DEC-2000; 2000US-0251856.
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PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0255678.

(HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465570/50.
DR N-PSDB; AAL01332.
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen
is used in preventing, treating or ameliorating a medical condition

XX Claim 11; SEQ ID NO 4020; 1297pp + Sequence listing; English.

CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a protein of the invention.

XX Sequence 173 AA;

Query Match 37.6%; Score 362; DB 22; Length 173;
Best Local Similarity 42.9%; Pred. No. 3.6e-30;
Matches 75; Conservative 35; Mismatches 55; Indels 10; Gaps 3;

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QY 73 ICRVSTSPAKDSIFEDELFLDLVSFSDTATPDIKSHYAFRIFDDEGDTLNREDLSRLV 132
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QY 133 NCLTGEEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVISRSPDEASSF 187
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RESULT 10
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ID AAM43637 standard; Protein; 173 AA.

AC AAM43637;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 315.

XX Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmologic; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antiulcer; vulnerrary; anticonvulsant; antibacterial;
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.

OS Homo sapIens.

XX WO200155308-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01309.

XX 31-JAN-2000; 2000US-0179065.
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PR 27-SEP-2000; 2000US-0235834.
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PR 01-DEC-2000; 2000US-0250391.
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PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
MPI; 2001-488781/53.
N-PSDB; AAI63943.

New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders -

Claim 11; SEQ ID NO 315; 664bp + Sequence Listing; English.

The invention relates to human polynucleotides (AAI63803-AAI64012) and the encoded proteins (AAM434497-AAM43660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly

CC	from WIPo at ftp.wipo.int/pub/published_pcl_sequences.
XX	Sequence 173 AA;
SO	Query Match 37.6%; Score 362; DB 22; Length 173; Best Local Similarity 42.9%; Pred. No. 3.6e-30; Matches 75; Conservative 35; Mismatches 55; Indels 10; Gaps
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OY	73 ICRVFTSPAKDLSFEDEFLDLVSFSDTATPDIKSHVAFRIFFDDGDTLNREDLSRLV 13
Db	57 ICRVFS--HKGMFSFEDVLGMASVFSEQACPSLKIEYAFRIYDFNENGFIDEEDLQRII 11
OY	133 NCLTGEEDTRLASASEMKOLIDNILEESDIDRDGTINSEFQHVISRSPDFASSF 187
Db	114 LRLNSDD--MSEDLMDLTNNHVLXSDDLNDNDMLSFSEFEHAMAKSPDFMTPF 165
RESULT 11	
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ID	AAU19952 standard; Protein; 173 AA.
XX	AAU19952;
AC	
XX	06-DEC-2001 (first entry)
DT	
XX	Novel human calcium-binding protein #61.
DE	
XX	
KW	Human; calcium-binding protein; calcium flux; neurological disease;
KW	immune dysfunction; digestive disorder; neoplastic disease;
KW	blood disorder; infectious disease; gene therapy; immunosuppressive;
KW	antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
KW	virucide.
XX	
OS	Homo sapiens.
XX	
PN	WO200155304-A2.
XX	
PD	02-AUG-2001.
PF	17-JAN-2001; 2001WO-US01302.
XX	
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PR	07-JUN-2000; 2000US-0209467.
PR	28-JUN-2000; 2000US-0214886.
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PR	07-JUL-2000; 2000US-0216880.
PR	11-JUL-2000; 2000US-0217487.
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PR	14-AUG-2000; 2000US-0225270.
PR	14-AUG-2000; 2000US-0225447.
PR	14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 25-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.

PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465568/50.

N-PSDB; AAS31637.

Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition -
Claim 11; SEQ ID No 149; 542pp; English.

The present invention relates to the isolation of novel human calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic sequences encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amyotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SCID), digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AAU19892-AAU19969 represent the novel human calcium-binding proteins.
CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 173 AA;

Query Match 37.6%; Score 362; DB 22; Length 173;
Best Local Similarity 42.9%; Pred. No. 3.6e-30;
Matches 75; Conservative 35; Mismatches 55; Indels 10; Gaps 3;

QY 13 LAEYQDLTFLTKQELLHAHRRCELLPOEQRTVESSLRAQVPFEQILSLPELKANPFKER 72
 Db 1 LEEYQALTFELTRNEILCIHDTFLKLCPPGKYKEATL---TMDQVSSILPALRVNPFDR 56
 QY 73 ICRVSTSPAKSLSFEDFLDLVSFSDTATPDIKSHYAFRIEFDDEDDGTINREDLSRLV 132
 Db 57 ICRVFS--HKMSEFEDVLGMASVSEQACPSLKIYAFRIYDFENGFIDEEDLQRII 113
 QY 133 NCLTGEEDTRLASASEMKQILDNILEESDIDRDGTINLSEFQHVISRSPDEASSF 187
 Db 114 LRLNSTD--MSEDLMLDTNHLVLSXSDLDNDNMLSFSEFEHAMAKSPDEMTPF 165

RESULT 12
 AAE09736
 ID AAE09736 standard; Protein; 187 AA.
 AC AAE09736;
 XX
 DT 29-NOV-2001 (first entry)
 DE Human kinase interacting protein.
 KW Human; kinase interacting protein; novel human protein; NHP;
 KW gene therapy; drug screening; mental disorder; biological disorder;
 KW medical disease; nootropic.
 OS Homo sapiens.
 PN WO200166760-A2.
 PD 13-SEP-2001.
 PF 08-MAR-2001; 2001WO-US07499.
 PR 08-MAR-2000; 2000US-0187719.
 PA (LEXI-) LEXICON GENETICS INC.
 PI Mathur B, Turner CA;
 DR WPI; 2001-557870/62.
 DR N-PSDB; AAD16796.

PT Novel polynucleotides encoding human kinase interacting protein useful
 PT for drug screening, diagnosis and in gene therapy of biological
 PT disorders -
 XX
 PS Claim 2; Page 31-32; 32pp; English.

CC The present amino acid sequence is a novel human protein (NHP),
 CC human kinase interacting protein. NHP oligonucleotides are useful
 CC as hybridisation probes for screening libraries and assessing gene
 CC expression patterns. Sequences derived from regions adjacent to the
 CC intron/exon boundaries of NHP gene are used to design primers for
 CC use in amplification assays to detect mutations within the exons,
 CC splice sites, introns that can be used in diagnostics and
 CC pharmacogenomics. NHP nucleotide sequences are useful for drug
 CC screening and nucleotide construct encoding NHP products are
 CC useful in gene therapy for modulating NHP expression and to produce
 CC genetically engineered host cells to express NHP products in vivo.
 CC The encoded NHP polypeptides are useful for generating antibodies,
 CC as reagents in diagnostic assays, for identifying other cellular
 CC gene products related to NHP and as reagents in assays for screening
 CC for compounds that are useful in the treatment of mental, biological
 CC or medical disorders and diseases.

Query Match 35.9%; Score 345; DB 22; Length 187;
 Best Local Similarity 40.4%; Pred. No. 2.5e-28;
 Matches 78; Conservative 42; Mismatches 61; Indels 12; Gaps 5;

QY 1 MGGSGSRLSKELLAAYQDLTFLTKQELLHAHRRCELLPO---EQRTVESSLRAQVPE 56
 Db 1 MGNKQTVFTHQOLEAYQDCTFFTRKEIMRLFYRYQDLAPQLVPLDYTTCPD--VKVPE 57
 QY 57 QILSLPELKANPFKERICRVSTSPAKSLSFEDFLDLVSFSDTATPDIKSHYAFRIED 116
 Db 58 LIGSMPELKNPFRQIAQVFS-EDGDGHMTLDNFMFSVMSEMAPRDLKAYAFKIYD 116
 QY 117 FDDGTINREDLSRLVNCLTGEGEDTRLASASEMKQILDNILEESDIDRDGTINLSEFQHV 176
 Db 117 FNNDDYICAWDLEQTYTKLT-RGE--LSAEFVSLVCEKVLDEADGDHGRSLSEDFQNM 172
 QY 177 ISRSPDFASSFKI 189
 Db 173 ILRAPDFLSTFHI 185

RESULT 13
 ABB64325
 ID ABB64325 standard; Protein; 206 AA.
 AC ABB64325;
 XX
 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 19767.
 DE Drosophila; developmental biology; cell signalling; insecticide;
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 OS Drosophila melanogaster.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PF 23-MAR-2001; 2001WO-US09231.
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 PA (PEKE) PE CORP NY.
 PI Venter JC, Adams M, Li PWD, Myers EW;
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL08428.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 19767; 21pp + Sequence Listing; English.
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

Query Match 35.7%; Score 343.5; DB 22; Length 206;
 Best Local Similarity 44.3%; Pred. No. 4.1e-28;
 Matches 78; Conservative 30; Mismatches 51; Indels 17; Gaps 5;

QY 17 QDLTFLTKQELLHAHRRCELLPO---EQRTVESSLRAQVPFEQILSLPELKANPFKERI 73

Db 43 KDCFTETRKELRVHKKRRELRLPDLVPRQMTGEGASSVKVPCECIEKMPELR----- 94
QY 74 CRVESTPAKDSLSFEDFLDLISVSFSDTATPDIKSHYAFRIPEFDDGTLNREDSRLVN 133
Db 95 -EAFSRD-GGGNLSFEDFLDALSVEQAPRDIVYAFKIYDFDQDGFIGHAD---LMS 149
QY 134 CLTGEEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFOHVISRSPDFASGFKI 189
Db 150 CLTMTKN-ELSPHEHQIADKVIIEADVDDGKLSILEFHVILRAPDFLSTFHI 204
RESULT 14
ABP41194
ID ABP41194 standard; Protein; 169 AA.
XX
AC ABP41194;
XX
DT 23-AUG-2002 (first entry)
XX
DE Human ovarian antigen HTLHN94, SEQ ID NO:2326.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX
OS Homo sapiens.
XX
PN WO200200677-A1.
XX
PD 03-JAN-2002.
XX
PF 07-JUN-2001; 2001WO-US18569.
XX
PR 07-JUN-2000; 2000US-209467P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-147878/19.
DR N-PSDB; ABQ54271.
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g.
PT ovarian cancer), immune disorders, cardiovascular disorders and
PT neurological diseases -
XX
PS Claim 11; SEQ ID NO 2326; 2922bp; English.
XX
CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),

CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 169 AA;
QY 64 LKANPFEKRICRVESTPAKDSLSFEDFLDLISVSFSDTATPDIKSHYAFRIPEFDDGTL 123
Db 47 LQENPFKERIVAAFS-EDGEGNLTENDFVDMFSVLCESAPRELKANYAFKIYDFNTDNEI 105
QY 124 NREDLSRLVNCLTGEEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFOHVISRSPDF 183
Db 106 CKEDLELTARLT---KSELDEEVVLVCDKVIIEADLDGDKLGAFDFEDMAKAPDF 161
QY 184 ASSEFKI 189
Db 162 LSTFHI 167

RESULT 15
AA11976
ID AA11976 standard; Protein; 120 AA.
XX
AC AA11976;
XX
DT 18-JUN-1999 (first entry)
XX
DE Human 5' EST secreted protein SEQ ID NO: 576.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide; prostate;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition.
XX
OS Homo sapiens.
XX
PN WO9906550-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-IB01232.
XX
PR 01-AUG-1997; 97US-0905144.
XX
PA (GEST) GENSET.
XX
PI Duclert A, Dumas Mline Edwards J, Lacroix B;
XX
DR WPI; 1999-153780/13.
DR N-PSDB; AAX40698.
XX
PT New isolated prostate-derived nucleic acids - used to develop
PT products which may have cytokine, immune regulatory, haematopoiesis
PT regulating, anti-inflammatory or tumour inhibition activity
XX
PS Claim 34; Page 664; 675pp; English.

CC AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins expressed in prostate, and encode the proteins
CC given in AY11716 to AY11993 respectively. The proteins given represent
CC the signal peptide and an N-terminal fragment of a secreted protein. The
CC nucleic acid sequences can be used for producing secreted human gene
CC products. They can also be used to develop products for diagnosis and
CC therapy. The proteins obtained may have cytokine activity, cell
CC proliferation and differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptides can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell.
XX

XX
SQ Sequence 120 AA;

Query Match 22.9%; Score 220; DB 20; Length 120;
Best Local Similarity 66.2%; Pred. No. 2.3e-15;
Matches 45; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

OY 1 MGGSGSRLSKELLAEXODLTLTKQELLAHRRCELLPQEQRTVESSLRAQVFEQILS 60
DB 1 MGGSGSRLSKELLAEXODLTLTKQELLAHRRCELLPQEQRTVESSLRAQVFEQILS 60
OY 61 LPELKANP 68
DB 61 FGSSRPTP 68

Search completed: November 21, 2002, 17:59:33
Job time : 36 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 21, 2002, 17:57:51 ; Search time 12 Seconds

(without alignments)
660.165 Million cell updates/sec

Title: US-09-878-454A-2

Perfect score: 962

Sequence: 1 MCGSGSRLSKELLAEXQDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	962	100.0	191	1	KIP1_HUMAN
2	909	94.5	191	1	KIP1_MOUSE
3	908	94.4	191	1	KIP1_RAT
4	345	35.9	187	1	KIP2_MOUSE
5	343	35.7	187	1	KIP2_HUMAN
6	216.5	22.5	177	1	CALB_NAEGR
7	210.5	21.9	174	1	CALB_SCHPO
8	199.5	20.7	174	1	CALB_NEUCR
9	199.5	20.7	174	1	CALB_YEAST
10	186.5	19.4	169	1	CALB_MOUSE
11	186.5	19.4	169	1	CALB_MOUSE
12	178.5	18.6	170	1	CALC_DROME
13	178	18.5	194	1	CA22_MOUSE
14	174.5	18.1	170	1	CALB_DROME
15	173	18.0	194	1	CA22_HUMAN
16	172.5	17.9	178	1	CALC_MOUSE
17	171.5	17.8	186	1	FREQ_DROME
18	170.5	17.7	175	1	CALC_RAT
19	166.5	17.3	189	1	NCS2_CAEEL
20	158	16.4	190	1	APIC_APLICA
21	152.5	15.9	195	1	H520_HUMAN
22	151	15.7	189	1	NCS1_HUMAN
23	151	15.7	189	1	NCS1_XENLA
24	146	15.2	190	1	NCS1_CAEEL
25	146	15.2	192	1	VIS3_CHICK
26	146	15.2	192	1	VIS3_MOUSE
27	145	15.1	192	1	VIS3_HUMAN
28	140	14.6	189	1	NCAH_DROME
29	137	14.2	190	1	VIS2_RAT
30	136.5	14.2	214	1	TESC_HUMAN
31	136	14.1	192	1	NCAD_MOUSE
32	135	14.0	192	1	HIPP_HUMAN
33	131	13.6	192	1	NCAD_CHICK

34	130.5	13.6	172	1	CATR_MOUSE	P41209 mus musculu
35	130.5	13.6	214	1	TESC_MOUSE	Q9JK15 mus musculu
36	130	13.5	192	1	NCAD_HUMAN	P29554 homo sapien
37	130	13.5	192	1	NECX_APLICA	Q16982 aplysia cal
38	130	13.5	791	1	KDGG_HUMAN	P49619 homo sapien
39	129	13.4	189	1	NCS1_SCHPO	Q09711 schizosacch
40	128	13.3	190	1	VIS1_HUMAN	P28677 homo sapien
41	128	13.3	804	1	KDGB_HUMAN	Q9Y6T7 homo sapien
42	127.5	13.3	172	1	CAT2_HUMAN	Q12798 homo sapien
43	126.5	13.1	195	1	H520_MOUSE	Q9D869 mus musculu
44	124.5	12.9	801	1	KDGB_RAT	P49621 rattus norv
45	124	12.9	189	1	NCS1_YEAST	Q06389 saccharomyc

ALIGNMENTS

RESULT 1
KIP1_HUMAN
ID KIP1_HUMAN STANDARD; PRT; 191 AA.
AC Q99828; 000735; 000693; Q99971; Q96J54;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
DE interacting protein) (Kinase interacting protein) (KIP) (CIB) (SNK
DE interacting protein 2-28) (SIP2-28).
GN CIB1 OR PRKDCIP OR KIP OR CIB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuan O.;
RT "SNK, a Ser/Thr protein kinase, associated proteins.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98040126; PubMed=9372844;
RA Wu X., Lieber M.R.;
RT "Interaction between DNA-dependent protein kinase and a novel protein,
RT KIP.";
RL Mutat. Res. 385:13-20(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=97184102; PubMed=9030514;
RA Naik U.P., Patel P.M., Parise L.V.;
RT "Identification of a novel calcium-binding protein that interacts
RT with the integrin alpha1b cytoplasmic domain.";
RL J. Biol. Chem. 272:4651-4654(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20284952; PubMed=10826701;
RA Hattori A., Seki N., Hayashi A., Kozuma S., Saito T.;
RT "Genomic structure of mouse and human genes for DNA-PKcs interacting
RT protein (KIP).";
RL DNA Seq. 10:415-418(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP STRUCTURE BY NMR OF 9-191.
RX MEDLINE=20283154; PubMed=10822252;
RA Hwang P.M., Vogel H.J.;
RT "Structures of the platelet calcium- and integrin-binding protein and
RT the alpha1b-integrin cytoplasmic domain suggest a mechanism for
RT calcium-regulated recognition; homology modelling and NMR studies.";
RL J. Mol. Recognit. 13:83-92(2000).
CC -I- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-

```
CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
CC CYTOPLASMIC DOMAIN.
CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK.
CC -1- TISSUE SPECIFICITY: UBQUITOUS.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
DR EMBL; U83236; AAB39758.1; -
DR EMBL; U85611; AAB53387.1; -
DR EMBL; U82226; AAC51106.1; -
DR EMBL; AB021866; BAA36281.1; -
DR EMBL; BC000846; AAH00846.1; -
DR PDB; 1DGV; 08-DEC-99.
DR Genew; HGNC:16920; CIB1.
DR MIM; 602293; -
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 2.
DR ProDom; PD000012; EF-hand; 1.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; 2.
KW Calcium-binding; Repeat; 3D-structure.
FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
FT CA_BIND 161 172 EF_HAND 2 (POTENTIAL).
FT CONFLICT 44 44 T -> S (IN REF. 3 AND 5).
FT SEQUENCE 191 AA; 21717 MW; 9AA6EA7897881E55 CRC64;
SQ
Query Match 100.0%; Score 962; DB 1; Length 191;
Best Local Similarity 100.0%; Pred. No. 4.3e-70;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSGSRSLKELLAEYODLFLTKQELLAAHRRFCELLPQQRVTESSLRVQVFQQLIS 60
Db 1 MGSGSRSLKELLAEYODLFLTKQELLAAHRRFCELLPQQRVTESSLRVQVFQQLIS 60
QY 61 LPELKANPEKERICRVSTSPAKDSLSEDFDLDSVSDTATPDIKSHYAFRIEDFDD 120
Db 61 LPELKANPEKERICRVSTSPAKDSLSEDFDLDSVSDTATPDIKSHYAFRIEDFDD 120
QY 121 GTLNREDLSRLVCLTGEGETRLSASEMKQLIDNILESDIDRDGTINLSEFQHYISRS 180
Db 121 GTLNREDLSRLVCLTGEGETRLSASEMKQLIDNILESDIDRDGTINLSEFQHYISRS 180
QY 181 PDFASSEKIVL 191
Db 181 PDFASSEKIVL 191
RESULT 2
KIP1_MOUSE
ID KIP1_MOUSE STANDARD; PRT; 191 AA.
AC O920F4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
DE interacting protein) (Kinase interacting protein) (KIP) (CIB).
GN CIB1 OR PRKDCIP OR KIP OR CIB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
```

```
RX MEDLINE-99069785; PubMed-9852683;
RA Seki N., Hayashi A., Abe M., Araki R., Fujimori A., Fukumura R.,
RA Hattori A., Kozuma S., Ohlira M., Hori T., Saito T.;
RT "Chromosomal assignment of the gene for human DNA-PKcs interacting
RT protein (KIP) on chromosome 15q25.3-q26.1 by somatic hybrid analysis
RT and fluorescence in situ hybridization."
RL J. Hum. Genet. 43:275-277(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Fetal kidney;
RX MEDLINE-99160477; PubMed-10051332;
RA Saito T., Seki N., Hattori A., Hayashi A., Abe M., Araki R.,
RA Fujimori A., Fukumura R., Kozuma S., Matsuda Y.;
RT "Structure, expression profile, and chromosomal location of a mouse
RT gene homologous to human DNA-PKcs interacting protein (KIP) gene."
RL Mamm. Genome 10:315-317(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Naik M.U., Naik U.P.;
RT "Cloning and tissue distribution of murine calcium and integrin
RT binding protein, CIB."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [5]
RP FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
RX IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
CYTOPLASMIC DOMAIN (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
CC SIMILARITY).
CC -1- TISSUE SPECIFICITY: UBQUITOUS.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
DR EMBL; AB006463; BAA74429.1; -
DR EMBL; AB017361; BAA36165.1; -
DR EMBL; AF173010; AAG38960.1; -
DR EMBL; AK010345; BAB26868.1; -
DR HSSP; Q99828; 1DGV.
DR MGD; MGI:1344418; C1b1.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 2.
DR ProDom; PD000012; EF-hand; 1.
```

DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127
 FT CA_BIND 161 172
 SO SEQUENCE 191 AA; 21763 MW; C85B603A19F9D9AC CRC64;

Query Match 94.58; Score 909; DB 1; Length 191;
 Best Local Similarity 94.28; Pred. No. 7.2e-66;
 Matches 180; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAETDFTLTKEILLAHRRFCCLPQEQRTVESSLRAQVPEQILS 60
 DB 1 MGGSGSRLSKELLAETDFTLTKEILLAHRRFCCLPQEQRTVESSLRAQVPEQILS 60
 QY 61 LPELKANPKEKICRVSTSPAKDSLSFEDFLDLSVSDTATPDIKSHYAFRIEDDD 120
 DB 61 LPELKANPKEKICRVSTSPAKDSLSFEDFLDLSVSDTATPDIKSHYAFRIEDDD 120
 QY 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNILESDIDRDGTINLSEFOHVISRS 180
 DB 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNILESDIDRDGTINLSEFOHVISRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 3

KIP1_RAT
 ID KIP1_RAT STANDARD; PRT; 191 AA.

AC Q9R010;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
 interacting protein) (Kinase interacting protein) (KIP) (CIB).
 GN CIB1 OR PRKDCIP OR KIP OR CIB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99452760; PubMed-10523297;
 RA Kauselmann G., Weller M., Wulff P., Jessberger S., Konietzko U.,
 RA Scafield J., Staudl U., Bereliter-Hahn J., Streibhardt K., Kuhl D.;
 RT "The polo-like protein kinases Pnk and Snk associate with a Ca(2+)-and
 RT integrin-binding protein and are regulated dynamically with synaptic
 RT plasticity.";
 RL EMBO J. 18:5528-5539(1999).

CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
 CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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DR EMBL; AF136585; AAF08368.1; -
 DR HSSP; Q99828; 1DGV.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 2.
 DR ProDom; PD000012; EF-hand; 1.

DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127
 FT CA_BIND 161 172
 SO SEQUENCE 191 AA; 21800 MW; 3B0B0228879FCC7 CRC64;

Query Match 94.48; Score 908; DB 1; Length 191;
 Best Local Similarity 94.28; Pred. No. 8.7e-66;
 Matches 180; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAETDFTLTKEILLAHRRFCCLPQEQRTVESSLRAQVPEQILS 60
 DB 1 MGGSGSRLSKELLAETDFTLTKEILLAHRRFCCLPQEQRTVESSLRAQVPEQILS 60
 QY 61 LPELKANPKEKICRVSTSPAKDSLSFEDFLDLSVSDTATPDIKSHYAFRIEDDD 120
 DB 61 LPELKANPKEKICRVSTSPAKDSLSFEDFLDLSVSDTATPDIKSHYAFRIEDDD 120
 QY 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNILESDIDRDGTINLSEFOHVISRS 180
 DB 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNILESDIDRDGTINLSEFOHVISRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 4

KIP2_MOUSE
 ID KIP2_MOUSE STANDARD; PRT; 187 AA.

AC Q9Z309;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kinase interacting protein 2 (KIP 2).
 GN KIP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Brain, and Testis;
 RX MEDLINE-99132027; PubMed-9931475;
 RA Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Hori T.,
 RA Saito T.;
 RT "Structure, expression profile and chromosomal location of an isolog
 RT of DNA-PKcs interacting protein (KIP) gene.";
 RL Biochim. Biophys. Acta 1444:143-147(1999).

CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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DR EMBL; AB016080; BAA36545.1; -
 DR HSSP; Q99828; 1DGV.
 DR MGI; 1929293; KIP2.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 3.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 DR KIP2
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127
 FT CA_BIND 157 168
 SO SEQUENCE 187 AA; 21703 MW; D21D21DCBDB6F5C CRC64;

Query Match	35.98;	Score 345;	DB 1;	length 187;
Best Local Similarity	37.84;	Pred. No. 6.6e-21;		
Matches	73;	Conservative 43;	Mismatches 65;	Indels 12;
				Gaps 4;

QY	1	MGSGSRLSKELLA	EYODLFTLKQ	ELLAHRRFCE---	LLPQQRIV	ESSLRQVPFE	56
		:	:	:	:	:	
		:	:	:	:	:	
Db	1	MGNKQITFTEQ	LDNYQDC	CFENKKDILKLH	ARFYE	LAPNLPVNDYR--	KSPIVHPMS 57
		:	:	:	:	:	
		:	:	:	:	:	
QY	57	QILSLPELKANP	FERICRV	STSPAKDSLS	FEDFLDL	SVFSDTATPD	IKSHYAFRIED 116
		:	:	:	:	:	
		:	:	:	:	:	
Db	58	LIQMPBELREN	PFKERIVEA	FS EDGEGNLT	FTNFVDM	FSVLCESAP	RELKANYAFKIYD 116
		:	:	:	:	:	
		:	:	:	:	:	
QY	117	FDDDGTLNR	EDLSRLVNC	LGTGEGED	TRL	SASEMKOLIDN	ILEESDIDRDGTINLSEFOHV 176
		:	:	:	:	:	
		:	:	:	:	:	
Db	117	FNTDNFICK	EDLEMTL	ARLT---	KSELEDE	EVVLVCDK	YIEADLDGDGKLGFADEFDM 172
		:	:	:	:	:	
		:	:	:	:	:	
QY	177	ISRSPDFA	SSFKI	189			
		:	:	:			
		:	:	:			
Db	173	IAKAPD	FLSTFHI	185			
		:	:	:			
		:	:	:			

```

RESULT 5
KIP2_HUMAN
ID KIP2_HUMAN STANDARD; PRT; 187 AA.
AC 075838;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kinase interacting protein 2 (KIP 2).
GN KIP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RC MEDLINE=99132027; PubMed=9931475;
RA Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Hori T.,
RA Saito T.;
RT "Structure, expression profile and chromosomal location of an isolog
RT of DNA-PKcs interacting protein (KIP) gene.";
RT Blochm. Biophys. Acta 1444:143-147(1999).
RL -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
CC DR EMBL; AB012955; BAA33584.1; -.
CC DR HSSP; Q99828; IDGV.
CC DR MIM; 605564; -.
CC DR InterPro; IPR002048; EF-hand.
CC DR Pfam; PF00036; efhand; 3.
CC DR ProDom; PD000012; EF-hand; 1.
CC DR SMART; SM00054; EFh; 2.
CC DR PROSITE; PS00018; EF_HAND; 2.
KW Calcium-binding; Repeat.
FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
FT CA_BIND 157 168 EF_HAND 2 (POTENTIAL).
FT FT SEQUENCE 187 AA; 21643 MW; D51F6C25AD381BEF CRC64;
SQ

Query Match 35.7%; Score 343; DB 1; Length 187;
Best Local Similarity 37.8%; Pred. No. 9.6e-21;
Matches 73; Conservative 43; Mismatches 65; Indels 12; Gaps 4;

1 MGGSGSRLSKELAEYODLTFLTKOELLAAHRCF-----LLPQEQRTVSSSLRAQVPE 56
II:::IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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Db      1  MGKNOQITFTEEQLDNYQDCTEFFNKDKILKHSRFYELAPNLVPM DYR--KSPIVHV PMS 57
QY      57  QIISLPPELKANPEKERICRVFSTSPAKDSLSEFEDFLDLVSFSDTATPDIKSHYAFRIED 116
          |::|||:|||||||  ||  ::::| ||::|:|  |  ::::|::|::|:|
Db      58  LIIOPELRENPEKERIVAAFS-EDGEGNLTENDEFVDMFSVLCESAPRELKANYAFKIYD 116
QY      117 FDDDGTLNREDSLRLVNCLTGEGEDTRLSASEMKOLIDNILEESDIDRDGTINLSEFOHV 176
          |::|::|::|::|  |  |  ::::|:|  |  |  ::::|:|  |  |  ::::|:
Db      117 FNTDNFICKEDLELTARLT---KSELDEEEVVLVCDKVIIEADLDGDGKGFADFE DM 172
QY      177 ISRSPDEASSFKI 189
          |:::|||||  |  |
Db      173 IAKAPDELSTFHI 185

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ID	CALB_NAEGR	STANDARD	PRT	177 AA
AC	P42322;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)			
DE	(Calcineurin regulatory subunit).			
GN	CNBL.			
OS	Naegleria gruberi.			
OC	Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.			
OX	NCBI_TaxID=5762;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-NEG;			
RX	MEDLINE-95172399; Pubmed-7867946;			
RT	Remillard S.P., Lai E.Y., Levy Y.Y., Fulton C.;			
RT	"A calcineurin-B-encoding gene expressed during differentiation of the amoeboid flagellate Naegleria gruberi contains two introns.";			
RL	Gene 154:39-45(1995).			
CC	-1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM SENSITIVITY (BY SIMILARITY).			
CC	-1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY SUBUNIT (B) (BY SIMILARITY).			
CC	-1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING SITES (BY SIMILARITY).			
CC	-1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.			
CC	-----			
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CC	-----			
DR	EMBL; U04380; AAA81896.1; .			
DR	HSSP; P06705; LAUI.			
DR	InterPro; IPR002048; EF-hand.			
DR	Pfam; PF00036; efhand; 4.			
DR	ProDom; PD000012; EF-hand; 2.			
DR	SMART; SM00054; EFh; 4.			
DR	PROSITE; PS00018; EF_HAND; 4.			
KW	Calcium-binding; Repeat.			
FT	CA_BIND 38 49 EF_HAND 1 (BY SIMILARITY).			
FT	CA_BIND 70 81 EF_HAND 2 (BY SIMILARITY).			
FT	CA_BIND 107 118 EF_HAND 3 (BY SIMILARITY).			
FT	CA_BIND 148 159 EF_HAND 4 (BY SIMILARITY).			
SQ	SEQUENCE 177 AA; 20057 MW; 01D4A48E6947E97C CRC64;			
QY	1 MGSGSRLSKELLAETDITFLTKQETLLAHRFCCLLPQORTVSSLRQVPEQILS 60			


```
Db 1 MGNTSSLRPEVEEMQKGTNETOKEIKLYKREKKLDKDGNGTISK-----DEFLM 52
QY 61 LPELKANPEKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIEDDDD 120
Db 53 IPELAVNPFLVKRIVSIFDEN-GDGSVNFKEETIALSVFNAQGDQKRLFEAFKYYDIDGD 111
QY 121 GTLNREDLSRLVNCLTGEGEDTRLASASEMKQLIDNILESDIDRDGTINLSEFQHVIS 178
Db 112 GYISNGELFVYLMKMGV-----NNLSVDVQLQIVDKTILEADEDDGDKISFEFAKTLIS 165

RESULT 7
CALB_SCHPO
ID CALB_SCHPO STANDARD; PRT; 174 AA.
AC Q9U93;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)
DE (Calcineurin regulatory subunit).
GN CNB1 OR SPC830.06.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks R., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RA "The genome sequence of Schizosaccharomyces pombe.";
RT Nature 415:871-880(2002).
RL Nature 415:871-880(2002).
CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERNS CALCIUM
CC SENSITIVITY (BY SIMILARITY).
CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
CC SUBUNIT (B) (BY SIMILARITY).
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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DR EMBL; AL109850; CAB52879.1; -
DR HSSP; P06705; 1AUI.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efnad; 4.
DR PRINTS; PR00450; RECOVERIN.
DR Prodom; PD000012; EF-hand; 1.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF-HAND; 4.
KW Calcium-binding; Myristate.
FT CA_BIND 34 45 EF-HAND 1 (BY SIMILARITY).
FT CA_BIND 66 77 EF-HAND 2 (BY SIMILARITY).
FT CA_BIND 103 114 EF-HAND 3 (BY SIMILARITY).
FT CA_BIND 144 155 EF-HAND 4 (BY SIMILARITY).
SQ SEQUENCE 174 AA; 19675 MW; EEF38FE74959442E CRC64;

Query Match 21.9%; Score 210.5; DB 1; Length 174;
Best Local Similarity 27.2%; Pred. No. 3.2e-10;
Matches 49; Conservative 46; Mismatches 68; Indels 17; Gaps 4;

QY 1 MGGSGSRSLKELLAEYODLFTLKQETLLAHRCELLPQEQRTVESSLRAQVPFEQILS 60
Db 1 MGQSQSQIFEDLISN---SSFSNEELIERIKRKF-----IDANQSGSIDRNEFLS 48
QY 61 LPELKANPEKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIEDDDD 120
Db 49 IPSVSNPLASRLFSVDEDDGGD-VDPQEFINSLSVFSVHGKNEKKLFKFIYDIDRD 107
QY 121 GTLNREDLSRLVNCLTGEGEDTRLASASEMKQLIDNILESDIDRDGTINLSEFQHVISRS 180
Db 108 GYISNGELVYLMKMGV-----TLNREDQLQIVDKTIMEVDKDRDGKISFEFKDIVSGS 163

RESULT 8.
CALB_NEUCR
ID CALB_NEUCR STANDARD; PRT; 174 AA.
AC P87072; O13408;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)
DE (Calcineurin regulatory subunit).
GN CNB-1 OR CAN-B.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74A;
RX MEDLINE=98007857; PubMed=9349701;
RA Prokisch H., Yarden O., Dleminger M., Tropschug M., Barthelmeß I.B.,
RA "Impairment of calcineurin function in Neurospora crassa reveals its
RA essential role in hyphal growth, morphology and maintenance of the
RA apical Ca2+ gradient.";
RT Mol. Gen. Genet. 256:104-114(1997).
RL Mol. Gen. Genet. 256:104-114(1997).
CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERNS CALCIUM
CC SENSITIVITY.
CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
CC SUBUNIT (B).
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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Db      1 GAAPSKIVDGLLED----TFNDRDEIERLKRFRMKLDRSSGSGSIDKN-----EFMSI 48
QY      62 PEIKANPEKERICRVFSTSPAKDLSFEDELDDLVSFSDTATPDIKSHYAFRIEDFDDG 1211
Db      49 FGVSNNPLAGRIMEVEFDADNSGD-VDFQEFITGLSIFSGSGSKDEKLRFPAFKIYDIDKDG 1077
QY      122 TLNREDLSRLVNCLTGEGEDTRLRSASEMKOLIDNILESDIDRDGTINLSEFOHVI 177
Db      108 FISNGELFIVLKIMVG-----SNLDEQLQOIYDRTIVENDSGDGRLSFEFEKNAI 159

RESULT 10
CALB_HUMAN
ID      CALB_HUMAN      STANDARD;      PRT;      169 AA.
AC      P06705; P15117; Q08044;
DT      01-JAN-1988 (Rel. 06, Create)
DT      01-APR-1990 (Rel. 14, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory
DE      subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform
DE      1).
GN      PPP3R1 OR CNB OR CNA2.
OS      Homo sapiens (Human).
OS      Bos taurus (Bovine), and
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606, 9913, 10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT      "Isolation and sequence of a cDNA clone for human calcineurin B, the
RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
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RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
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RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
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RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
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RT      phosphatase.";
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RX      MEDLINE=90126237; Pubmed=2558868;
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RL      DNA 8:675-682(1989).
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RC      SPECIES-Human;
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RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
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RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
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RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
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RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
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RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
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RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
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RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT      "Isolation and sequence of a cDNA clone for human calcineurin B, the
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RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
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RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
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RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
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RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
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RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT      "Isolation and sequence of a cDNA clone for human calcineurin B, the
RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
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RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT      "Isolation and sequence of a cDNA clone for human calcineurin B, the
RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT      "Isolation and sequence of a cDNA clone for human calcineurin B, the
RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
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RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT      "Isolation and sequence of a cDNA clone for human calcineurin B, the
RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT      "Isolation and sequence of a cDNA clone for human calcineurin B, the
RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
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RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT      "Isolation and sequence of a cDNA clone for human calcineurin B, the
RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT      "Isolation and sequence of a cDNA clone for human calcineurin B, the
RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT      "Isolation and sequence of a cDNA clone for human calcineurin B, the
RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES-Human;
RX      MEDLINE=90126237; Pubmed=2558868;
RA      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT      "Isolation and sequence of a cDNA clone for human calcineurin B, the
RT      Ca2+-binding sub
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RC SPECIES=Bovine;
RX MEDLINE=95360994; PubMed=7543369;
RA Griffith J.P., Kim J.L., Kim E.E., Stintchak M.D., Thomson J.A.,
RA Fitzgibbon M.J., Fleming M.A., Caron P.R., Hsiao K., Navia M.A.;
RT "X-ray structure of calcineurin inhibited by the immunophilin-
RT Immunosuppressant FKBP12-FK506 complex.";
RL Cell 82:507-522(1995).
[8]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RC SPECIES=Human;
RX MEDLINE=96097077; PubMed=8524402;
RA Kissinger C.R., Parge H.E., Knighton D.R., Lewis C.T., Pelleter L.A.,
RA Tempczyk A., Kalish V.J., Tucker K.D., Shewalter R.E., Moomaw E.W.,
RA Gastinel L.N., Habuka N., Chen X., Maldonado F., Barker J.E.,
RA Bacquet R., Villafraña J.E.;
RT "Crystal structures of human calcineurin and the human FKBP12-FK506-
RT calcineurin complex.";
RL Nature 378:641-644(1995).
CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
CC SENSITIVITY.
CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
CC SUBUNIT (B).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, 1 (SHOWN HERE) AND 2; ARE
CC PRODUCED BY ALTERNATIVE SPLICING IN RAT.
CC -1- TISSUE SPECIFICITY: ISOFORM 2 IS TESTIS-SPECIFIC.
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
DR EMBL; M30773; AAB08721.1; -
DR EMBL; X71666; CA50659.1; -
DR EMBL; L03554; AAA40854.1; -
DR EMBL; D14568; BAA03422.1; -
DR EMBL; D14425; BAA03318.1; -
DR PIR; A33391; A33391.
DR PIR; S34127; S34127.
DR PIR; J420297; JT0297.
DR PIR; S42716; S42716.
DR PIR; S42717; S42717.
DR PDB; 1AUI; 03-DEC-97.
DR PDB; 1TCC; 12-FEB-97.
DR Genew; HGNC:9317; PPP3R1.
DR MIM; 601302; -
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat; Alternative splicing; Myristate;
KW 3D-structure.
FT INIT_MET 0 0
FT LIPID 1 1 MYRISTATE.
FT CA_BIND 30 41 EF-HAND 1.
FT CA_BIND 62 73 EF-HAND 2.
FT CA_BIND 99 110 EF-HAND 3.
FT CA_BIND 140 151 EF-HAND 4.
FT VAASPLIC 1 1
FT CONFLICT 11 11
FT CONFLICT 153 153 C -> S (IN REF. 3).
FT SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;
Query Match 19.4%; Score 186.5; DB 1; Length 169;
Best Local Similarity 31.1%; Pred. No. 2.5e-08;

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Query Match.	19.4%;	Score 186.5;	DB 1;	Length 169
Best Local Similarity	31.1%;	Pred. No. 2.5e-08;		

	Matches	38;	Conservative	32;	Mismatches	47;	Indels	5;	Gaps	2;
QY	56	EQLSLPELKANDEKERICRVSTSPAKDSISFEDFLDLVSFSDDTATPDIKSHYAERIE	115	: : : : : :	: : : : :					
Db	40	EEFMSLPELQONPLVQRVIDIFDTD-GNGEVDYDFKEFIEGVSQFSVKGDKEQKLRAFAFRIV	98							
QY	116	DDEDDGTLNREDLSRLVNCLTGEGEDTRRSASEMKOLIDNILEESDIDRDGTINLSEFOH	175	: : : : :	: : : : : : :					
Db	99	DMDKDGYISNGELFYVLKMMVG---NNIKDTQLQQIVDKTIINADRKDGGRISFEFFCA	154							
QY	176	VI 177								
' Db	155	VV 156								

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RESULT 11
CALB_MOUSE STANDARD; PRT; 169 AA.
AC Q63810;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory
DE subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform
DE 1).
GN PPP3R1 OR CNB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN RN SEQUENCE FROM N.A..
RP TISSUE=Brain;
RC MEDLINE=92392379; PubMed=1325794;
RX Ueki K., Muramatsu T., Kincaid R.L.;
RA "Structure and expression of two isoforms of the murine calmodulin-
RT dependent protein phosphatase regulatory subunit (calcineurin B).";
RT Biochem. Biophys. Res. Commun. 187:537-543(1992).
CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
CC SENSITIVITY.
CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
CC SUBUNIT (B).
CC -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC.
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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CC EMBL; S43864; AAB23171.1; -.
CC HSSP; P06705; 1A0I.
DR MGD; MGI:107172; Ppp3r1.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat; Myristate.
FT INIT_MET 0
FT LIPID 1
FT CA_BIND 30 41 EF_HAND 1.
FT CA_BIND 62 73 EF_HAND 2.
FT CA_BIND 99 110 EF_HAND 3.
FT CA_BIND 140 151 EF_HAND 4.
SEQUENCE 169 AA; 19142 MW; D1490BA5BD2F432F CRC64;

```

	Query Match	19.4%;	Score 186.5;	DB 1;	Length 169;	
	Best Local Similarity	31.1%;	Pred. No. 2.5e-08;			
	Matches	38;	Conservative 32;	Mismatches 47;	Indels 5;	Gaps
QY	56	EQLSLPELKANPFEKERICRVFSTSPAKDSISFEDELILLSVFSDTATPDIKSHYAFRIF	115			
		: : : : : : : : : :				
Dd	40	EEFMSPLELQNPNLVQRVIDIFTD-GNGEVDKEFIIEGVSQSFKGDKEQKLRFAFRIV	98			
QY	116	DFDDDGTLNREDSLRLVNCLTGEGEDTRLASSEMKKOLIDNILLESDDIRDRGTINLSFQH	175			
		: : : : : : : : : :				
Dd	99	DMDKDEGISNGELLEQVLKMVG---NNLKDTQLQQIIVDKTIINADKKGDDRISFEERCA	154			
QY	176	VI 177				
		: :				
Dd	155	VV 156				

RESULT	12
CALC_DROME	STANDARD; PRT; 170 AA.
ID	024214; Q9V315;
AC	01-NOV-1997 (Rel. 35, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DE	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Calcineurin B subunit, isoform 2 (Protein phosphatase 2B regulatory subunit).
GN	CANB2 OR CNB2 OR CG11217.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Canton-S;
RX	MEDLINE=97080515; PubMed=8921860;
RA	Warren W.D., Phillips A.M., Howells A.J.;
RT	"Drosophila melanogaster contains both X-linked and autosomal
RL	homologues of the gene encoding calcineurin B.";
RN	Gene 177:149-153(1996).
RP	[2]
RC	SEQUENCE FROM N.A.
RX	STRAIN=Berkley;
RA	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA	Foster C., Gabrieltian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: CALCINEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING
CC PROTEIN FOUND IN ALL CELLS FROM YEAST TO MAMMALS, IT IS A CALCIUM
CC DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY
CC SIMILARITY).
CC -1- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B), THE A COMPONENT IS
CC THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM
CC SENSITIVITY (BY SIMILARITY).
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.

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DR EMBL; U56245; AAC47350.1; -
DR EMBL; AE003840; AAF59195.1; ALT_SEQ.
DR HSSP; P06705; LTCO.
DR FlyBase; FBgn0015614; CanB2.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR PRODOM; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat.
FT CA_BIND 31 42 EF_HAND 1 (POTENTIAL).
FT CA_BIND 63 74 EF_HAND 2 (POTENTIAL).
FT CA_BIND 100 111 EF_HAND 3 (POTENTIAL).
FT CA_BIND 141 152 EF_HAND 4 (POTENTIAL).
SQ SEQUENCE 170 AA; 19267 MW; FDB1BD9DB5A4BDEC CRC64;

Query Match 18.6%; Score 178.5; DB 1; Length 170;
Best Local Similarity 24.7%; Pred. No. 1.1e-07;
Matches 44; Conservative 43; Mismatches 72; Indels 19; Gaps 4;

QY 3 GSGSLSKELLAAYQDLTFLEKQELLAAHRRFCCLLPQEQRTVESSLRAQVFEQILSLP 62
Db 2 GNETSIPMEKCSNFD-----ADEIRRLGKRF-----RKLDLNSGALSYDEFMSLP 47

QY 63 ELKANPEKERICRVFSTSPAKDSLSFEFDLDSVFSDTATPDIKSHYAFRIFFDDGT 122
Db 48 ELQONPLVQVIDIFD-ADNGEVDYFKEFIQGSQFSVKGDKLSKLRAFRITDMNDGY 106

QY 123 LNRDELRLVNCITGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVISRS 180
Db 107 ISNGELFOVLKMMVG-----NNLKDTQLQIVDKITGFADKDEDGKISFDEFCSVVGNT 160

RESULT 13
CA22_MOUSE STANDARD; PRT; 194 AA.
AC Q62877;
DT 01-NOV-1997 (Rel. 35, Created).
DT 01-NOV-1997 (Rel. 35, Last sequence update).
DT 15-JUN-2002 (Rel. 41, Last annotation update).
DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin

DE homologous protein) (S1d470).
GN CHP.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; TISSUE=Liver;
RX MEDLINE=96215311; PubMed=8626580;
RA Barroso M.R., Bernd K.K., Dewitt N.D., Chang A., Mills K.,
RA Szul E.S.,
RT "A novel Ca2+-binding protein, p22, is required for constitutive
RT membrane traffic.";
RL J. Biol. Chem. 271:10183-10187(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; TISSUE=Brain;
RX MEDLINE=21374135; PubMed=11481038;
RA Matsumoto M., Miyake Y., Nagita M., Inoue H., Shtakubo D.,
RA Takemoto K., Ohtsuka C., Murakami H., Nakamura N., Kanazawa H.,
RT "A serine/threonine kinase which causes apoptosis-like cell death
RT interacts with a calcineurin B-like protein capable of binding Na+/H+
RT exchanger.";
RL J. Biochem. 130:217-225(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RA Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Saito T.,
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse; STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
CC -1- PTM: BOTH N-MYRISTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL
CC CHANGES ARE ESSENTIAL FOR ITS FUNCTION.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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CC or send an email to license@isb-sib.ch).

DR EMBL; U39875; AAB04146.1; -
DR EMBL; AB070350; BAB63369.1; -
DR EMBL; AB025217; BAA84688.1; -

QY 86 LSFEDLDLLSVSDTATPDIKSHYAFRIEDDDGTLNREDSRLVNCLTGEGEDTRL 145
 Db 70 VDEKEFIQVGSQFSVRGDKLSKLRFAFRYDMNDGYISNGELFQVLMVAVG-----NNLK 125
 QY 146 ASEMROLIDNILEESDIDRDGTINLSEFOHVISR 180
 Db 126 DTOLQIVDKTICFADKDEDEKISFDEFCVVGNT 160

RESULT 15
 CA22_HUMAN
 ID CA22_HUMAN STANDARD: PRT; 194 AA.
 AC 099653;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin homologous protein) (Calcineurin B homolog).
 GN CHP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-B-cell;
 RX MEDLINE=97057295; PubMed=8901634;
 RA Lin X., Barber D.L.;
 RT "A calcineurin homologous protein inhibits GTPase-stimulated Na-H exchange."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:12631-12636(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Muscle;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC (BY SIMILARITY). INHIBITS GTPASE-STIMULATED NA-H EXCHANGE. SPECIFICALLY BINDS TO THE SODIUM/HYDROGEN EXCHANGER 1 (NHE1) AT A DOMAIN THAT IS CRITICAL FOR GROWTH FACTOR STIMULATION OF EXCHANGE ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED. HAS BEEN FOUND IN FETAL EYE, LUNG, LIVER, MUSCLE, HEART, KIDNEY, THYMUS AND SPLEEN.
 CC -1- PTM: BOTH N-MYRISTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL CHANGES ARE ESSENTIAL FOR ITS FUNCTION IN EXOCYTIC TRAFFIC (BY SIMILARITY).
 CC -1- PTM: PHOSPHORYLATED IN VIVO. DECREASE IN ITS PHOSPHORYLATION IS ASSOCIATED WITH AN INCREASE IN EXCHANGE ACTIVITY. THE PHOSPHORYLATION STATE MAY REGULATE THE BINDING TO NHE1.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC -----
 DR EMBL; U61538; AAB37770.1; -
 DR EMBL; BC001646; AAH01646.1; -
 DR HSSP; P06705; IADI.
 DR MIM; 606988;
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 3.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
 KW Calcium-binding; Repeat; Myristate; phosphorylation.
 FT INIT_MET 0
 FT LIPID 0
 FT DOMAIN 1 1 MYRISTATE (BY SIMILARITY).
 FT 38 49 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).

FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
 FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
 FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
 SQ SEQUENCE 194 AA; 22325 MW; 17DDEE5F03C88380 CRC64;
 Query Match 18.0%; Score 173; DB 1; Length 194;
 Best Local Similarity 26.3%; Pred. No. 3.6e-07;
 Matches 51; Conservative 35; Mismatches 76; Indels 32; Gaps 6;
 QY 5 GSR-----LSKLLAEYQDLFELTKQELLAHRRFCCELLPQEQRYESSSLRAQVPFEQILS 60
 Db 1 GSRASTLLRDELEIEIKKETGFSHSQITRLYSRFTSLDKGNGTISR-----EDFQR. 52
 QY 61 LPELKANPEKERICRVFSTSPAKDSLSFEDLDLSVF-----SDTATPD----- 105
 Db 53 IPELAINPLGDRILINAFPE-GEQVNFGRFMRTLAHFRPIEDNEKSKDVNGPEPLNSRS 111
 QY 106 IKSHYAFRIEDFDDGTLNREDSRLVNCLTGEGEDTRLASSEMROLIDNILEESDIDRD 165
 Db 112 NKLHFAFRLYLDLKDDEKISRDELLQVLRMVG-----VNISDEQLGSIADRTIQEADQDGD 167
 QY 166 GTINLSEFOHVISR 179
 Db 168 SAISFTEFVKLEK 181

Search completed: November 21, 2002, 17:58:12
 Job time : 12 secs

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OM protein - protein search, using sw model

Run on: November 21, 2002, 17:57:51 ; Search time 17 Seconds
(without alignments)
1080.099 Million cell updates/sec

Title: US-09-878-454A-2

Perfect score: 962
Sequence: 1 MGGSGSRLSKELLAEXDYL.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413	42.9	311	2	T21563 hypothetical prote
2	210.5	21.9	174	2	T41632 probable calcineur
3	204.5	21.3	175	2	JH0462 phosphoprotein pho
4	199.5	20.7	174	2	T47245 calcineurin regula
5	186.5	19.4	170	1	A33391 calcineurin regula
6	186.5	19.4	170	1	S34127 calcineurin regula
7	186.5	19.4	170	1	JC1220 calcineurin regula
8	186.5	19.4	216	1	S42716 calcineurin regula
9	183.5	19.1	369	2	T22708 hypothetical prote
10	178.5	18.6	170	2	JC5174 calcineurin regula
11	175.5	18.2	170	2	JC7242 calcineurin regula
12	174.5	18.1	170	2	A44307 calcineurin regula
13	172.5	17.9	179	2	JC1221 calcineurin regula
14	170.5	17.7	165	2	PS0261 calcineurin regula
15	170.5	17.7	176	2	JQ1232 calcineurin regula
16	170.5	17.7	195	2	T28047 calcineurin regula
17	170.5	17.7	213	2	T31775 calcineurin regula
18	166.5	17.3	190	2	T20725 hypothetical prote
19	164.5	17.1	226	2	T51357 calcineurin B-like
20	156	16.2	190	2	I51686 calcineurin B-like
21	152.5	15.9	226	2	T08923 calcineurin B-like
22	151.5	15.7	213	2	T51356 calcineurin B-like
23	151	15.7	193	2	JH0816 neural vishin-lik
24	151	15.7	193	2	I50676 gene Rem-1 protein
25	151	15.7	246	2	T05308 hypothetical prote
26	151	15.7	246	2	H85387 hypothetical prote
27	150	15.6	193	2	S47565 calcium-binding pr
28	148	15.4	192	2	T01375 calcium sensor hom
29	145	15.1	190	2	A55666 neurocalcin - fru1

30	142	14.8	191	2	JH0815 neural vishin-lik
31	141	14.7	270	2	JC7631 K+ channel-interac
32	138.5	14.4	254	2	T29566 hypothetical prote
33	138	14.3	193	2	JC2186 hippocalcin - huma
34	137	14.2	224	2	F96668 protein FIN19.5 (l
35	135	14.0	193	2	JH0616 hippocalcin (clone
36	135	13.9	195	2	S58303 hippocalcin - rat
37	134	13.9	190	2	JH0605 related to neurona
38	133	13.8	191	2	JH0605 neural vishin-lik
39	133	13.8	191	2	A48979 vishin-lik prote
40	130.5	13.6	172	2	S38531 caltractin - mouse
41	130	13.5	791	2	A53691 diacylglycerol kin
42	129	13.4	190	2	S61168 hypothetical prote
43	127.5	13.3	172	2	I38424 centrin - human
44	126.5	13.1	202	2	S21155 recoverin - mouse
45	126	13.1	151	2	A71409 calmodulin 8 (limpo

ALIGNMENTS

RESULT 1
T21563
hypothetical protein F30A10.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T21563
R;Barlow, K.
submitted to the EMBL Data Library, October 1996
A/Reference number: Z19442
A/Accession: T21563
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-311 <WIL>
A/Cross-references: EMBL:Z81072; PIDN:CAB03019.1; GSPDB:GN00019; CESP:F30A10.1
A/Experimental source: clone F30A10
C/Genetics:
A/Gene: CESP:F30A10.1
A/Map position: 1
A/Introns: 106/2; 139/3; 190/3; 240/1

Query Match 42.9%; Score 413; DB 2; Length 311;
Best Local Similarity 42.5%; Pred. No. 8.3e-25;
Matches 88; Conservative 41; Mismatches 52; Indels 26; Gaps 5;

QY 1 MGGSGSRLS-----KELLAEXDYLTLFKOELLAAHRCCELLPQEQRYESS 48
DB 111 MGNASSLSSELNLFSGGVFTREQLDEYODCTFFTRKDILRYKRYALNPHK---VPTN 167
QY 49 LRAQVP-----FEQILSPELKANPFKERICRVFSNPAKDSLSFEDFLDLSVFSDTA 102
DB 168 MQGNRPATITTLTFEEVEKMPKELKENPFKRRICEVFS-EDGRGNLSFDDFLDMFSVSEMA 226
QY 103 TPDIKSHYAFRIFFDDDDGTLNREDSLRLVNCILGEGEDTRLASASEMKQILDNILEESDI 162
DB 227 PLQLKLYAFRIYDGDDELLGHDLKMRSLTRD---ELSDVEVEFIERIIEEADL 282
QY 163 DRDGTINLSEFQHVISRSPDFASSFKI 189
DB 283 DGDSSINFAEFHVSRSDFIRTFHI 309

RESULT 2
T41632

probable calcineurin b subunit - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000
C/Accession: T41632
R;McDougall, R.M.; Rajandream, M.A.; Barrell, B.G.; Ramsperger, U.; Pohl, T.
submitted to the EMBL Data Library, August 1999
A/Reference number: Z22005
A/Accession: T41632
A/Status: preliminary; translated from GB/EMBL/DBJ

[illegible]

A;Molecule type: DNA
A;Residues: 1-175 <MA1>
A;Cross-references: EMBL:Z28190; NID:g486336; PIDN:CAA82034.1; MIPS:YKLJ
A;Experimental source: strain S288C
R;Wieman, S.; Voss, H.; Schwaeger, C.; Rupp, T.; Stegemann, J.; Zimmermann, J.; Grotl
submitted to the EMBL Data Library, July 1993
A;Description: Sequencing and analysis of 51.5 kilobases on the left arm of chromosome
A;Reference number: S34679
A;Accession: S34680
A;Molecule type: DNA
A;Residues: 31-175 <WI2>
A;Cross-references: EMBL:X74151; NID:g450365; PIDN:CAA52248.1; PID:g395235
A;Experimental source: strain S288C
R;Pardo, J.M.
submitted to the EMBL Data Library, September 1993
A;Description: The protein phosphatase calcineurin is essential for NaCl tolerance in
A;Reference number: S52281
A;Accession: S52282
A;Molecule type: DNA
A;Residues: 1-175 <PAR>
A;Cross-references: EMBL:Z26521; NID:g473144; PIDN:CAA81290.1; PID:g473146
C;Genetics:
A;Gene: SGD:CNB1; YCN2
A;Cross-references: SGD:S0001673; MIPS:YKL190w
A;Map position: 11L
A;Introns: 18/1
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; 11
F;2-175/Product: phosphoprotein phosphatase regulatory chain #status predicted <MAT>
F;21-52/Domain: calmodulin repeat homology <EF1>
F;53-85/Domain: calmodulin repeat homology <EF2>
F;90-122/Domain: calmodulin repeat homology <EF3>
F;131-163/Domain: calmodulin repeat homology <EF4>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status experimental

```

Query Match      21.3%; Score 204.5; DB 2; Length 175;
Best Local Similarity 27.1%; Pred. No. 5.8e-09;
Matches 48; Conservative 44; Mismatches 68; Indels 17; Gaps 4;

OY 1 MCGSGSRLSKELLAEXODLFTLTQKEILLAHRRFCCELLPQEQRTVESLSRAQVPFEQILS 60
   || : : : : || : : : : || : : : : || : : : : || : : : : || : : : :
DB 1 MGAAPSKIVDGLLED----TNFDRDEIERLRKRFRMKLRDSSGSIDKN-----EFMS 48

OY 61 LPELKANPFKERICRWFNSPAKDSLSFEDFLDLSVFSPTATPDIKSHYAFRIEDFDDD 120
   : : : : || : : : : : : : : : : : : : : : : : : : : : : : :
DB 49 IPGVSSNPLAGRIMEVFADNSGD-VDFQEFITGLSIFSGSGSKDEKLRFKITYDIDKD 107

OY 121 GTLNREDLSRLVNCLTGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQHVI 177
   | : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 108 GFISNGELFIVLKIMVG----SNLDDEQLQIQIVDRTIVENDSDGDGRLSFEEFKNAI 160

RESULT 4
T47245
calcineurin regulatory chain [imported] - Neurospora crassa
C/Species: Neurospora crassa
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 26-May-2000
C/Accession: T47245
R:Dieminger, M.; Tropischug, M.
submitted to the EMBL Data Library, April 1997
A/Reference number: Z24421
A/Accession: T47245
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-174 <DIE>
A/Cross-references: EMBL:Y12814; PIDN:CAA73345.1
A/Experimental source: strain 74 A
C/Genetics:
A/Gene: Can B
C/Superfamily: calmodulin; calmodulin repeat homology
C/Keywords: EF hand

Query Match      20.7%; Score 199.5; DB 2; Length 174;

```

Best Local Similarity 26.1%; Pred. No. 1.4e-08;
Matches 41; Conservative 42; Mismatches 61; Indels 13; Gaps 3;
QY 24 KOEILAHRRFCELLPQEQRTVESSLRAQVFEQILSLPELKANPFKERICRVSTSPAK 83
Db 20 REEVDRLRKRFMKLDKDNSTIER-----EFLSLPQISTNPLATRMIAIFDENGCG 71
QY 84 DSLSEFEDFLDLVSFSDTATPDIKSHAFRIFFDDGTLNREDISRLVNCLTGEGEDTR 143
Db 72 D-VDFQEFVSGLSAFSRKGNKEQKLRFKRYVDIDRDGYISNGELFVLKMMVG----SN 126
QY 144 LSASEMKQLIDNILESDIDRDGTINLSEFQHVISR 180
Db 127 LKDDQLQRIVDKTIMEADLDKDGISFEETKMENT 163

RESULT 5
A33391
calcineurin regulatory chain - human
N/Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
C/Species: Homo sapiens (man)
C/Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Jul-1999
C/Accession: A33391
R/Guerini, D.; Krinks, M.H.; Sikele, J.M.; Hahn, W.E.; Klee, C.B.
DNA 8, 675-682, 1989
A/Title: Isolation and sequence of a cDNA clone for human calcineurin B, the Ca(2+)-binding protein
A/Reference number: A33391; MUID:90126237; PMID:2558868
A/Accession: A33391
A/Molecule type: mRNA
A/Residues: 1-170 <GUE>
A/Cross-references: GB:M30773; NID:g180704; PIDN:AAB08721.1; PID:g180705
C/Genetics:
A/Gene: GDB:PPP3R1; CALNB
A/Cross-references: GDB:136804; OMIM:601302
A/Map position: 2p16-2p15
C/Complex: heterodimer with calcineurin catalytic chain
C/Superfamily: calmodulin; calmodulin repeat homology
C/Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; 11pof
F:2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Modified site: aspartic acid (Asn) #status predicted
F:31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status predicted
F:63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status predicted
F:100,102,104,106,111/Binding site: calcium (Asp, Asp, Tyr, Glu) #status predicted
F:141,143,145,147,152/Binding site: calcium (Asp, Asp, Arg, Glu) #status predicted
Query Match 19.4%; Score 186.5; DB 1; Length 170;
Best Local Similarity 31.1%; Pred. No. 1.4e-07;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;
QY 56 EQILSLPELKANPFKERICRVSTSPAKDSLSEFEDFLDLVSFSDTATPDIKSHAFRI 115
Db 41 EEFMSLPQLQNPVQRYVIDFDTD-GNGEVDFKEFIEGVSQFSVKGDKEQKLRFARIRY 99
QY 116 DEDDGTLNREDLSRLVNCLTGEGEDTRLASASEMKQLIDNILESDIDRDGTINLSEFQ 175
Db 100 DMDKDGYSNGELFQVLKMMVG-----NNLKDTQLQIQIVDKTIINADKDGGRISFEFCA 155
QY 176 VI 177
Db 156 VV 157
RESULT 6
S34127
calcineurin regulatory chain [validated] - bovine
N/Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
C/Species: Bos primigenius taurus (cattle)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Sep-2000

C/Accession: I45831; JT0297; S34127
R/Nargang, C.E.; Bottorff, D.A.; Adachi, K.
DNA Seq. 4, 313-318, 1994
A/Title: Isolation and characterization of a cDNA clone coding for the calcium-binding protein
A/Reference number: I45831; MUID:95102111; PMID:7803816
A/Accession: I45831
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-170 <NA2>
A/Cross-references: EMBL:X71666; NID:g312968; PIDN:CAA50659.1; PID:g312969
R/Altken, A.; Klee, C.B.; Cohen, P.
Eur. J. Biochem. 139, 663-671, 1984
A/Title: The structure of the B subunit of calcineurin.
A/Reference number: JT0297; MUID:84132092; PMID:6321184
A/Accession: JT0297
A/Molecule type: protein
A/Residues: 2-11, 'M', 13-153, 'S', 155-169 <AIT>
R/Griffith, J.P.; Kim, J.L.; Kim, E.E.; Shtuchak, M.D.; Thomson, J.A.; Fitzgibbon, J.
Submitted to the Brookhaven Protein Data Bank, August 1996
A/Reference number: A66708; PDB:1TCO
A/Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 2-170
R/Griffith, J.P.; Kim, J.L.; Kim, E.E.; Shtuchak, M.D.; Thomson, J.A.; Fitzgibbon, J.
Cell 82, 507-522, 1995
A/Title: X-ray structure of calcineurin inhibited by the immunophilin-immunosuppressant cyclosporin A
A/Reference number: A56967; MUID:95360994; PMID:7543369
A/Contents: annotation; X-ray crystallography, 2.5 angstroms
C/Complex: heterodimer with calcineurin catalytic chain (see PIR:A56968)
C/Superfamily: calmodulin; calmodulin repeat homology
C/Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; 11pof
F:2-170/Product: calcineurin regulatory chain #status experimental <MAT>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status experimental
F:3/Modified site: aspartic acid (Asn) #status predicted
F:31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status experimental
F:63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status experimental
F:100,102,104,106,111/Binding site: calcium (Asp, Asp, Tyr, Glu) #status experimental
F:141,143,145,147,152/Binding site: calcium (Asp, Asp, Arg, Glu) #status experimental

Query Match 19.4%; Score 186.5; DB 1; Length 170;
Best Local Similarity 31.1%; Pred. No. 1.4e-07;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;
QY 56 EQILSLPELKANPFKERICRVSTSPAKDSLSEFEDFLDLVSFSDTATPDIKSHAFRI 115
Db 41 EEFMSLPQLQNPVQRYVIDFDTD-GNGEVDFKEFIEGVSQFSVKGDKEQKLRFARIRY 99
QY 116 DEDDGTLNREDLSRLVNCLTGEGEDTRLASASEMKQLIDNILESDIDRDGTINLSEFQ 175
Db 100 DMDKDGYSNGELFQVLKMMVG-----NNLKDTQLQIQIVDKTIINADKDGGRISFEFCA 155
QY 176 VI 177
Db 156 VV 157
RESULT 7
JC1220
calcineurin regulatory chain, brain - mouse
N/Alternate names: calcineurin beta-1 subunit; calcineurin chain B-1; phosphoprotein
C/Species: Mus musculus (house mouse)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: JC1220
R/Ueki, K.; Muramatsu, T.; Kincaid, R.L.
Biochem. Biophys. Res. Commun. 187, 537-543, 1992
A/Title: Structure and expression of two isoforms of the murine calmodulin-dependent protein kinase II
A/Reference number: JC1220; MUID:92392379; PMID:1325794
A/Accession: JC1220
A/Molecule type: mRNA
A/Residues: 1-170 <UEK>
A/Cross-references: GB:S43864; NID:g255078; PIDN:AAB23171.1; PID:g255079

F;128-160/Domain:	calmodulin repeat homology <EF4>	
F;2/Modified site:	myristylated amino end (Gly) (in mature form)	#status predicted
F;3/Modified site:	aspartic acid (Asn)	#status predicted

Query Match	18.6%;	Score 178.5;	DB 2;	Length 170;
Best Local Similarity	24.7%;	Pred. No. 5.8e-07;		
Matches 44;	Conservative 43;	Mismatches 72;	Indels 19;	Gaps 4;

```
OY      3 GSGSRLSKELLAEYQDFTFLTKOEILLAHRRFCELLPQEORTVLESSLRAQVPFEQILSLP 62
        | : : | : : :    ||          | ::         : :: :|||
Db      2 GNETSLPMEMCSNFD-----ADEIRRLGKRFE-----RKLDIDNSGALSVDEIMSLP 47
```

Qy 63 ELKANPEKERICRVFSTSPAKDSLSFEFDLLSVFSOTAFPDIKSHYAFRIEFDDEGCT 122
||: || :|: :| :|::|: :| ||
Db 48 ELOONPLVORVIDIFD-ADNGENYEDEKEFIGOVSOFSVGDKSLRFAFRITYMDMNGY 106

```
0Y      123 LNREDISRLVNCITGEGEDTFRLSASEMKOLIDNILEESDIDRDGTINLSEFQHYIERS 180
        :: : | :::: | ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db      107 ISNGELFOVLKMAVG---NNLKDTOLOOIIVDKTTIGFADKDEDGKISFEDEFCSYVNT 160
```

RESULT 11
JC7242

calcineurin regulatory subunit, calcineurin B - scallop (Patinopecten yessoensis)
N;Alternate names: Ca2+/calmodulin-dependent phosphoprotein phosphatase regulatory subunit
C;Species: Patinopecten yessoensis (Yesso scallop)
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C;Accession: J07242; PC7070
R:Uryu, M.; Nakatomi, A.; Watanabe, M.; Hatsuse, R.; Yazawa, M.
T. Biochem. 127, 739-746, 2000

A: Molecule type: mRNA
A: Title: Molecular cloning of cDNA encoding two subunits of calcineurin from scallop testis
A: Reference number: JC7241
A: Accession: JC7242

A;Cross-references: DDBJ:AB041524
A;Experimental source: testis
A;Accession: PC7070

A;Molecule type: protein
A;Residues: 12-68;73-85;92-170 <UR2>
C;Comment: This protein, one of Ca2+/calmodulin-dependent enzyme, is a testis-specific 1 to the regulation of filarial nematode.

C;Genetics:
A;Gene: *cnb*
C;Superfamily: calmodulin repeat homology
;Keywords: calcium binding, myosin, calcium, myosin

Query Match	18.28;	Score 175.5;	DB 2;	Length 170;
Best Local Similarity	25.18;	Pred. No. 9.9e-07;		
Matches	44;	Concomitant	41	

```
QY      3 GSGSRISKELLAEYODLFTLKQEIILAHRRFCELLPQEORTVESSLRAOVFFEQILSLP 62
        | : : | | : :          ||         | : :           : : : :||
q       3 CAVENOT DIVERGENT      .....::.....
```

63 EIKANPEKERICRVSTGSPAKDLSFEDFLDLLSVFSDTATPDIKSHYAFRTFDDEDDGT 122

```

123 LNREDLRLVNCILTEGEDTRLSASEMKOIIDNILEESDIDRDTINLSEFQHYI 177
      ::||:::|      |:::|:::|:::|:::|:::|:::|:::|:::|:::|
107 TAVSTTAVSTTAVSTTAVSTTAVSTTAVSTTAVSTTAVSTTAVSTTAVSTTAVST

```

RESULT 12

calcineurin regulatory chain 1 - fruit fly (*Drosophila melanogaster*)
 N; Alternate names: calcineurin beta subunit; calcineurin chain B-1; phosphoprotein phosph
 C; Species: *Drosophila melanogaster*

C;Accession: A44307
R;Guerint, D.; Montell, C.; Klee, C.B
J. Biol. Chem. 267, 22542-22549, 1992

A/Title: Molecular cloning and characterization of the genes encoding the two subunits of the *Ca*²⁺-ATPase from *Caenorhabditis elegans*
A/Reference number: A44307; MUID:93054551; PMID:1331060
A/Accession: A44307
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-170 <GUE>
A/Cross-references: GB:M97215; NID:g157048; PIDN:AAA28411.1; PID:g157049
A/Note: sequence extracted from NCBI backbone (NCBIP:117113)
C/Genetics:
A/Gene: FLYBase:CanB
A/Cross-references: FLYBase:FBgn0010014
C/Complex: heterodimer with calcineurin catalytic chain
C/Superfamily: calmodulin; calmodulin.repeat homology
C/Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer;
F/2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F/18-49/Domain: calmodulin repeat homology <EF1>
F/50-82/Domain: calmodulin repeat homology <EF2>
F/87-119/Domain: calmodulin repeat homology <EF3>
F/128-160/Domain: calmodulin repeat homology <EF4>
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/3/Modified site: aspartic acid (Asn) #status predicted

Query Match	18.1%;	Score 174.5;	DB 2;	Length 170;
Best Local Similarity	26.5%;	Pred. No. 1.2e-06;		
Matches 41;	Conservative 38;	Mismatches 63;	Indels 13;	Gaps 3

```

QY      26 EILAHRRFCELLPQORTVESSLRAQVPEEQILSLPELKANPFKERICRVFSTSPAKDS 85
      11      ::      | ::      : :: : :: ||| :: | : : : |
Db      19 EIRRLGRF-----RKLDLNSGASIDFEMSLPELOONPVRVOTIDFD-ADGNCF 69

```

```

OY      86 LSFEDFLDLVSFSDTATPDIKSHYAFRIFDDDGDTLNREDLSRLVNCITGEGEDTRL 145
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      70 VDFKEFTIOGVSQSVRGDKLSKLRPERFYDMNDGYISNGEFOVT KMMVG-----NNR K 125

```

```
QY 146 ASEMQLIDNILEESDIDRDGTINLSEFOHVISRS 180
      ::::: | : | | | | | : | :
Db 126 DTOLQOIYDKTICFADKDEGKISDEFFCSVGNLT 160
```

RESULT 13
JC1221

calcineurin regulatory chain, testis - mouse
NAlternate names: calcineurin beta-2 subunit; calcineurin chain B-2; phosphoprotein
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C/Accession: J01221
R/Dekl, K.; Muramatsu, T.; Kincaid, R.L.

A1:Title: Structure and expression of two isoforms of the murine calmodulin-depende
A:Reference number: JCI1220; MUID:92392379; PMID:1325794
A:Accession: JCI1221

A:Residues: 1-179 <UEK>
A:Cross-references: GB:543865; NID:g255080; PIDN:AAB23172.1; PID:g255081
A:Experimental source: testis

CiGenetics: A:Gene: PP2B-beta-2
CiComplex: heterodimer with calcineurin catalytic chain

C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; F;2-179/Product: calcineurin regulatory chain #status predicted <MAT> F;18-49/Domain: calmodulin repeat homology<EF1>

F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end(Gly) (in mature form) #status predicted

Query Match	17.9%;	Score 172.5;	DB 2;	Length 179;
Best Local Similarity	27.8%;	Pred. No. 1.8e-06;		
Matches 42;	Conservative 30;	Mismatches 66;	Indels 13;	Gaps 3;

A/Title: Molecular cloning and characterization of the genes encoding the two subunits of the *Ca*²⁺-ATPase from *Caenorhabditis elegans*
A/Reference number: A44307; MUID:93054551; PMID:1331060
A/Accession: A44307
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-170 <GUE>
A/Cross-references: GB:M97215; NID:g157048; PIDN:AAA28411.1; PID:g157049
A/Note: sequence extracted from NCBI backbone (NCBIP:117113)
C/Genetics:
A/Gene: FLYBase:CanB
A/Cross-references: FLYBase:FBgn0010014
C/Complex: heterodimer with calcineurin catalytic chain
C/Superfamily: calmodulin; calmodulin.repeat homology
C/Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer;
F/2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F/18-49/Domain: calmodulin repeat homology <EF1>
F/50-82/Domain: calmodulin repeat homology <EF2>
F/87-119/Domain: calmodulin repeat homology <EF3>
F/128-160/Domain: calmodulin repeat homology <EF4>
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/3/Modified site: aspartic acid (Asn) #status predicted

Query Match	18.1%;	Score 174.5;	DB 2;	Length 170;
Best Local Similarity	26.5%;	Pred. No. 1.2e-06;		
Matches 41;	Conservative 38;	Mismatches 63;	Indels 13;	Gaps 3

```

QY      26 EILAHRRFCELLPQORTVESSLRAQVPEEQILSLPELKANPFKERICRVFSTSPAKDS 85
      11      ::      | ::      : :: : :: ||| :: || : :: : |
Db      19 EIRRLGRF-----RKLDLNSGASIDFEMSLPELOONPVIORVTDIFD-ADGNCF 69

```

```

OY      86 LSFEDFLDLVSFSDTATPDIKSHYAFRIFDDDGDTLNREDLSRLVNCITGEGEDTRL 145
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      70 VDFKEFTIOGVSQSVRGDKLSKLRPERFYDMNDGYISNGEFOVT KMMVG----NNR K 125

```

```
QY 146 ASEMQLIDNILEESDIDRDGTINLSEFOHVISRS 180
      ::::: | : | | | | | : | :
Db 126 DTOLQOIYDKTICFADKDEGKISFDEFFCSVGNLT 160
```

RESULT 13
JC1221

calcineurin regulatory chain, testis - mouse
NAlternate names: calcineurin beta-2 subunit; calcineurin chain B-2; phosphoprotein
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C/Accession: J01221
R/Dekl, K.; Muramatsu, T.; Kincaid, R.L.

A1:Title: Structure and expression of two isoforms of the murine calmodulin-depende
A:Reference number: JCI1220; MUID:92392379; PMID:1325794
A:Accession: JCI1221

A:Residues: 1-179 <UEK>
A:Cross-references: GB:543865; NID:g255080; PIDN:AAB23172.1; PID:g255081
A:Experimental source: testis

CiGenetics: A:Gene: PP2B-beta-2
CiComplex: heterodimer with calcineurin catalytic chain

C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; F;2-179/Product: calcineurin regulatory chain #status predicted <MAT> F;18-49/Domain: calmodulin repeat homology<EF1>

F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end(Gly) (in mature form) #status predicted

Query Match	17.9%;	Score 172.5;	DB 2;	Length 179;
Best Local Similarity	27.8%;	Pred. No. 1.8e-06;		
Matches 42;	Conservative 30;	Mismatches 66;	Indels 13;	Gaps 3;

QY 35 CELLPEQ-----RTVESSLRAQVPFEQILSLPELKNPFKERICRVSTSPAKDSL 86
12 CNHFDQEEIRLQKSKFRKLDLDSGSLSEEFMRPELQNPVGRVIDIFDTD-GNGEV 70
QY 87 SFEDFLDLVSFSDTATPDIKSHYAFRIFFDDGDTLNREDLSRLVNCITGEGEDTRLISA 146
71 DHEFIVGTSGFSVKGEQKLRFAFRITDMDNDGFIISNGELFQVLKMMVG---NNLKD 126
QY 147 SEMKQIDNILEESDIDRDGTINLSEFQHY 177
Db 127 WQLQQLVDSKILVLKDGGRISFEESFSDV 157

RESULT 14

PS0261
calcineurin regulatory chain-like protein, testis - rat (fragment)
N/Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phospho
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Aug-1999
C/Accession: PS0261
R/Sugimoto, M.; Matsui, H.; Etoh, S.; Shimizu, T.; Nishio, H.; Mola, L.J.M.P.; Tokuda, M
Biochem. Biophys. Res. Commun. 180, 1476-1482, 1991
A/Title: Isolation and sequence of rat testis cDNA for a calcium binding polypeptide sim
A/Reference number: PS0261; MUID:92062183; PMID:1659420
A/Accession: PS0261
A/Molecule type: mRNA
A/Residues: 1-165 <SUG>
A/Cross-references: GB:S63991; NID:g238643; PIDN:AAB20281.1; PID:g238644
C/Superfamily: calmodulin; calmodulin repeat homology
C/Keywords: blocked amino end; calcium binding; duplication; EF hand
F/7-38/Domain: calmodulin repeat homology <EF1>
F/39-71/Domain: calmodulin repeat homology <EF2>
F/76-108/Domain: calmodulin repeat homology <EF3>
F/117-149/Domain: calmodulin repeat homology <EF4>

Query Match 17.7%; Score 170.5; DB 2; Length 165;
Best Local Similarity 31.1%; Pred. No. 2.3e-06;
Matches 38; Conservative 28; Mismatches 51; Indels 5; Gaps 2;

QY 56 EQILSLPELKNPFKERICRVSTSPAKDSLSEFEDFLDLVSFSDTATPDIKSHYAFRI 115
Db 30 DEFMSPLELQNPVGRVIDIFDTD-GNGEVDFREFIVGTSGFSVKGEQKLRFAFRIT 88
QY 116 DFDDGDTLNREDLSRLVNCITGEGEDTRLISASEMKQIDNILEESDIDRDGTINLSEFQ 175
Db 89 DMDNDGFIISNGELFQVLKMMVG---NNLKDWQLQQLVDSKILVLKDGGRISFEESFRD 144
QY 176 VI 177
Db 145 VV 146

RESULT 15

JQ1232

calcineurin regulatory chain-like protein - rat
N/Alternate names: calcineurin chain B-like protein

C/Species: Rattus norvegicus (Norway rat)

C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Jun-2000

C/Accession: JQ1232

R/Mukai, H.; Chang, C.D.; Tanaka, H.; Ito, A.; Kuno, T.; Tanaka, C.
Biochem. Biophys. Res. Commun. 179, 1325-1330, 1991

A/Title: cDNA cloning of a novel testis-specific calcineurin B-like protein.

A/Reference number: JQ1232; MUID:92028870; PMID:1718268

A/Accession: JQ1232

A/Molecule type: mRNA

A/Residues: 1-176 <MUK>

A/Cross-references: GB:D10393; GB:D90449; NID:g220687; PIDN:BA01232.1; PID:g220688

A/Experimental source: testis

A/Note: this protein appears to be expressed specifically in testis

C/Superfamily: calmodulin; calmodulin repeat homology

C/Keywords: blocked amino end; calcium binding; duplication; EF hand; lipoprotein; myris

F/2-176/Product: calcineurin regulatory chain-like protein #status predicted <MAT>
F/18-49/Domain: calmodulin repeat homology <EF1>

F/50-82/Domain: calmodulin repeat homology <EF2>
F/87-119/Domain: calmodulin repeat homology <EF3>
F/128-160/Domain: calmodulin repeat homology <EF4>
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/3/Modified site: aspartic acid (Asn) #status predicted

Query Match 17.7%; Score 170.5; DB 2; Length 176;
Best Local Similarity 31.1%; Pred. No. 2.5e-06;
Matches 38; Conservative 28; Mismatches 51; Indels 5; Gaps 2;

QY 56 EQILSLPELKNPFKERICRVSTSPAKDSLSEFEDFLDLVSFSDTATPDIKSHYAFRI 115
Db 41 DEFMSPLELQNPVGRVIDIFDTD-GNGEVDFREFIVGTSGFSVKGEQKLRFAFRIT 99
QY 116 DFDDGDTLNREDLSRLVNCITGEGEDTRLISASEMKQIDNILEESDIDRDGTINLSEFQ 175
Db 100 DMDNDGFIISNGELFQVLKMMVG---NNLKDWQLQQLVDSKILVLKDGGRISFEESFRD 155
QY 176 VI 177
Db 156 VV 157

Search completed: November 21, 2002, 18:00:18
Job time : 18 secs